

PA (AMGE-) AMGEN INC.
 XX Bosselman RA, Martin FH, Suggs SV, Zsebo KM.
 XX WPI: 1995-346090/45.
 DR N-PSDB; AAT04889.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 PS Disclosure: Fig 15C; 127pp; English.
 XX
 CC AAR83997 is human stem cell factor (SCF). Non-naturally occurring SCF
 CC and C-terminally truncated polypeptides stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem cells
 CC and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia, for
 CC enhancing engraftment of bone marrow during transplantation or for
 CC bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for the
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC
 SQ Sequence 208 AA;
 XX
 Query Match 100.0%; Score 1061; DB 16; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3,8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRTQWILTCIYQLLEFNPLVTEGICRNRYNNVKDVTKIVANLPKQWITLKYPG 60
 Db |||||||
 QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVCEKENS 120
 Db |||||||
 QY 61 mdvlpshcwisemvqvsldstldldkfsnysldklvinvdldvecvkenns 120
 Db |||||||
 QY 121 KDLSKFSPEPRRLTPEEFRRIRNRSIDAFKDPVVASSETSDCVVSTLSPEKDSRVSVT 180
 Db |||||||
 QY 121 kdlskfsksperrltpeeffirfnrsidafkdpvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSSNSKRYIYL 208
 Db |||||||
 QY 181 kpfmlpvaasslrndssssnskyiyl 208
 Db |||||||
 RESULT 2
 AAR95175
 ID AAR95175 standard; Protein: 208 AA.
 XX
 AC AAR95175;
 XX
 DT 03-OCT-1996 (first entry)
 XX
 DE Stem cell factor.
 XX
 DE Stem cell factor.
 XX
 KW Stem cell factor; SCF; splice variant; embryo implantation;
 KM in vitro fertilisation; IVF.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..25 Location/Qualifiers
 FT /label= Sig.peptide
 FT Protein 26..208
 FT /label= Mat.protein
 XX

PN W09614410-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 31-OCT-1995; 95WO-GB02547.
 XX
 PR 28-APR-1995; 95GB-0008618.
 PR 04-NOV-1994; 94GB-0022293.
 XX
 PA (ISTE) ARS APPLIED RES SYST HOLDING NV.
 XX
 PI Dellow KA, Sharkey AM, Smith SK;
 XX
 DR WPI: 1996-251760/25.
 DR N-PSDB; AAT29489.
 XX
 PT Stem cell factor comprising C-terminal sequence given in
 PT specification - useful to ensure correct development of
 PT pre-implantation embryos before implantation into subject
 XX
 PS Disclosure: Fig 2; 25pp; English.
 XX
 CC A DNA sequence (AAT29489) codes for human stem cell factor (SCF)
 CC (AAR95175). The full-length SCF transcript consists of 8 exons.
 CC A novel splice variant has been identified that appears to arise
 CC from the inclusion of a novel exon (see also AAT29488) between exons
 CC 3 and 4 of the gene. The resulting frameshift produces a novel
 CC SCF consisting of the first 39 amino acids of mature SCF followed
 CC by a 33-amino acid C-terminal region (AAR95174). The novel SCF is
 CC useful for ensuring correct development of pre-implantation embryos.
 CC
 SQ Sequence 208 AA;
 XX
 Query Match 100.0%; Score 1061; DB 17; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3,8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRTQWILTCIYQLLEFNPLVTEGICRNRYNNVKDVTKIVANLPKQWITLKYPG 60
 Db |||||||
 QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVCEKENS 120
 Db |||||||
 QY 61 mdvlpshcwisemvqvsldstldldkfsnysldklvinvdldvecvkenns 120
 Db |||||||
 QY 121 KDLSKFSPEPRRLTPEEFRRIRNRSIDAFKDPVVASSETSDCVVSTLSPEKDSRVSVT 180
 Db |||||||
 QY 121 kdlskfsksperrltpeeffirfnrsidafkdpvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSSNSKRYIYL 208
 Db |||||||
 QY 181 kpfmlpvaasslrndssssnskyiyl 208
 Db |||||||
 RESULT 3
 AAY53286
 ID AAY53286 standard; Protein: 208 AA.
 XX
 AC AAY53286;
 XX
 DT 27-JUL-2000 (first entry)
 XX
 DE Human stem cell factor protein sequence.
 XX
 DE Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; synergistic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 cancer.
 XX
 OS Homo sapiens.
 XX


```

Db      1 mktqtwlltcylqlllfnplvktegicrnrvtnvkdvtkivanlpkdymltlkypg 60
QY      61 MDVLPSCWISSEWVQVSDSLFDLDKFSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
Db      61 mdvlpschwisemwvqslsdldldkfnsiseglsnysiidklvinivddlvecvken 120
QY      121 KDLKSKFSPEPRFLFPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 kdllksfkspetrllfpeeffrfrnsidafkdfvasetsdcvssstlspkdsrvsvt 180
QY      181 KPFLMPVAAASLRNDSSSSNSKYIYLI 208
Db      181 kpflmpvaasslrndssssnskyilyli 208

RESULT 5
AAB98355
ID      AAB98355 standard; Protein; 208 AA.
AC      AAB98355;
XX
XX      21-AUG-2001 (first entry)
DT
DE      Human stem cell factor (SCF) protein SPO ID NO:46.
KW      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KM      gene therapy.
XX
XX      Homo sapiens.
OS
XX      US6207454-B1.
PN
XX      27-MAR-2001.
PD
XX      31-DEC-1998; 98US-0224681.
PE
XX      21-DEC-1993; 93US-0172329.
PR      24-MAY-1995; 95US-0449653.
PR      12-JAN-1998; 98US-0005893.
PR      25-NOV-1992; 92US-0982255.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX      WPI: 2001-366062/38.
DR      N-PSDB; AAH41341.
XX
XX      Enhancing efficiency of transfer of polynucleotide into a target
PT      mammalian cell in vitro, involves exposing cell that expresses a stem
PT      cell factor receptor to stem cell factor, and introducing
PT      polynucleotide into cell in vitro -
XX
XX      Claim 16; Fig 15C; 210pp; English.
PS
XX
XX      The present invention describes a method for enhancing (E) the
CC      efficiency of transfer of a polynucleotide (I) into a target mammalian
CC      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
CC      factor (SCF) receptor to a biologically active SCF, its analogue or
CC      fragment, which induces cell proliferation, and introducing (I) to (II)
CC      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
CC      into the cell. The method is useful for enhancing the efficiency of the
CC      transfer of a polynucleotide into a target mammalian cell in vitro.
CC      The method is useful in gene therapy techniques. AAH41301 to AAH41364
CC      and AAB98351 to AAB98390 represent sequences used in the exemplification
CC      of the present invention.
XX
XX      Sequence 208 AA;
SQ

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Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3,8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKKTQWTLTCIYQLLLFNPLVTEGICRNRYNNVKDYTKIVANLPKDYMTTLKYPG 60
Db      1 mktqtwlltcylqlllfnplvktegicrnrvtnvkdvtkivanlpkdymltlkypg 60
QY      61 MDVLPSCWISSEWVQVSDSLFDLDKFSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
Db      61 mdvlpschwisemwvqslsdldldkfnsiseglsnysiidklvinivddlvecvken 120
QY      121 KDLKSKFSPEPRFLFPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 kdllksfkspetrllfpeeffrfrnsidafkdfvasetsdcvssstlspkdsrvsvt 180
QY      181 KPFLMPVAAASLRNDSSSSNSKYIYLI 208
Db      181 kpflmpvaasslrndssssnskyilyli 208

RESULT 6
AAU02457
ID      AAU02457 standard; Protein; 208 AA.
AC      AAU02457;
XX
XX      29-AUG-2001 (first entry)
DT
DE      Human SCF (stem cell factor) protein encoded by SCF cDNA.
XX
XX      Human: stem cell factor; SCF; early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder.
XX
XX      Homo sapiens.
OS
XX
XX      Key      Location/Qualifiers
FH      Peptide      1..25
FT      Protein      /label= Signal_peptide
FT      /label= Mature_SCF
XX
XX      US6207417-B1.
PN
XX
XX      27-MAR-2001.
PD
XX      07-JUN-1995; 95US-0482918.
PE
XX      21-DEC-1993; 93US-0172329.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
XX      (ZSEB/) ZSEBO K M.
PA      (BOSS/) BOSSSELMAN R A.
PA      (SUGG/) SUGGS S V.
PA      (MART/) MARTIN F H.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX      WPI: 2001-298941/31.
DR      N-PSDB; AAS04121.
XX
XX      Novel nucleic acids encoding stem cell factor useful for treating
PT      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
PT      disease, kala azar, anaemia and septicemia -
XX
XX      Example 3; Fig 15C; 209pp; English.
PS

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CC The present sequence represents human SCF (stem cell factor) protein
 CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 CC
 SQ Sequence 208 AA:

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRTNNVNDVTKLVANLPKDYMITLKYPG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 mkkqtwtlctiyqlllfnplvktegicrnrvtnnvdklvnlpkdymitlkyppg 60
 QY 61 MDVLPSSHCHWISBMVYQSDSLTDLDFKFSNISEGLSNTSIIDKLVNIYVDLVECKENSS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 mdvlpschwisemvqysdsltldkfsniseqlsntsiidklvniyddlveckenss 120
 QY 121 KDLSKFSKSPERLTPPEFFRIFNRSIDAFKDFVVASETSCVVSSTLSPKDSRVSVT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 kdlskfskspeprltfpeeffriinrsidafrkdfvvasetscvvstlspekdsrvsvt 180
 QY 181 KPFLMPVAASSLRNDSSSSNSKRYIYL 208
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 kpflmpvaasslrndssssnskryiyl 208

RESULT 7

AAU02764 ID AAU02764 standard; Protein: 208 AA.

AC AAU02764;

XX 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) protein encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KM anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /Label= Signal_peptide

FT /Label= Mature_SCF

XX US6218148-B1.

PD 17-APR-2001.

PF 21-DEC-1993;

XX 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-042383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

XX (AMGE-) AMGEN INC.

PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;

DR WPI: 2001-281051/29.

DR N-PSDB; AAS04222.

PT Isolated DNA sequence, encoding polypeptide product useful for
 PT stimulating growth of early haematopoietic progenitor cells -
 PS
 XX Example 3; Fig 15C; 167pp; English.

CC The present sequence represents human SCF (stem cell factor) protein
 CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02761-AAU02765, AAU02770-AAU02775, AAU02797) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04218) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 CC
 SQ Sequence 208 AA:

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRTNNVNDVTKLVANLPKDYMITLKYPG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 mkkqtwtlctiyqlllfnplvktegicrnrvtnnvdklvnlpkdymitlkyppg 60
 QY 61 MDVLPSSHCHWISBMVYQSDSLTDLDFKFSNISEGLSNTSIIDKLVNIYVDLVECKENSS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 mdvlpschwisemvqysdsltldkfsniseqlsntsiidklvniyddlveckenss 120
 QY 121 KDLSKFSKSPERLTPPEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPKDSRVSVT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 kdlskfskspeprltfpeeffriinrsidafrkdfvvasetscvvstlspekdsrvsvt 180
 QY 181 KPFLMPVAASSLRNDSSSSNSKRYIYL 208
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 kpflmpvaasslrndssssnskryiyl 208

RESULT 8

AAAB73565 ID AAB73565 standard; Protein: 208 AA.

AC AAB73565;

XX 07-AUG-2001 (first entry)

DE Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KM anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

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FT      /label= Signal_peptide
FT      26..208
FT      Protein
FT      /label= Mature_SCF
XX
XX
XX      US6204363-B1.
XX
XX      20-MAR-2001.
XX
XX      25-NOV-1992; 92US-0982255.
XX
XX      10-APR-1991; 91US-0684535.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX      WPI: 2001-256683/26.
XX      N-PSDB; AAH23899.
XX
XX      New stem cell factor polypeptides and their analogs which stimulate
XX      growth of early hematopoietic progenitors, useful for treating aplastic
XX      anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX      disease
XX
XX      Claim 1; Fig 15C; 166pp; English.
XX
XX      The present sequence represents human SCF (stem cell factor) protein
XX      encoded by SCF cDNA. The present invention relates to novel stem cell
XX      factors (AAH23561-AAH23568, AAH23571-AAH23576) and the
XX      polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX      including early haematopoietic progenitor cells. The invention also
XX      describes SCF peptides (AAH23578-AAH23597) and the oligonucleotides
XX      (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX      sequences. The polynucleotide encoding SCF is useful for producing
XX      SCF and useful in gene therapy. It is useful for treating disorders
XX      involving blood cells such as myelofibrosis, metastatic carcinoma,
XX      acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX      Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX      sarcoidosis, military tuberculosis, disseminated fungus disease,
XX      fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX      pyridoxine deficiency, and hypopigmentation disorders such as
XX      piebaldism and vitiligo.
XX
XX      Sequence 208 AA:
SQ

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ID      AAB96940 standard; Protein; 208 AA.
XX
XX      AAB96940;
XX
XX      13-JUL-2001 (first entry)
XX
XX      Human stem cell factor SEQ ID NO: 46.
XX
XX      Homo sapiens.
XX
XX      Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX      gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX      neurological damage; intestinal damage; infertility; AIDS; SCID;
XX      severe combined immunodeficiency.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..25
XX      Protein /label= signal_peptide
XX      /label= mature_stem_cell_factor
XX
XX      US6207802-B1.
XX
XX      27-MAR-2001.
XX
XX      09-NOV-1994; 94US-0336728.
XX
XX      25-NOV-1992; 92US-0982255.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX      WPI: 2001-353108/37.
XX      N-PSDB; AAF89101.
XX
XX      Novel isolated non-human mammalian stem cell factor polypeptide
XX      stimulating growth of early haematopoietic progenitor cells, useful for
XX      treating aplastic anaemia, lymphoma, Letterer-Siwe disease, kala azar,
XX      sarcoidosis -
XX
XX      Disclosure; Fig 15C; 209pp; English.
XX
XX      The present invention provides the protein and coding sequences of
XX      mammalian stem cell factors (SCFs). These are capable of stimulating the
XX      growth of early haematopoietic progenitor cells, neural stem cells and
XX      primordial germ stem cells. The sequences are useful in the treatment of
XX      leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX      nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX      and intestinal damage, infertility, AIDS and severe combined
XX      immunodeficiency (SCID). The present sequence is an SCF described in the
XX      invention.
XX
XX      Sequence 208 AA:
SQ

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Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DB 121 KDLKSKFSKSPERLFTPEEFIRLFRSIDAFKDFVASETSCVVSSTLSPEKDSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
 DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 10

AA011710
 ID AAR11710 standard; Protein: 208 AA.

AC AAR11710;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= sig_peptide

FT Protein 26..208 /label= mat_protein

EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-0505548.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

DR WPI: 1991-119233/17.

DR N-PSDB; AA011540, AA011541.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have haematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

PS Disclosure; Fig 15C; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AA011509-Q11543.

XX Sequence 208 AA;

SO

Query Match

Best local similarity 99.2%; Score 1052; DB 12; Length 208;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWIIITCIYLLQLLEPLVKEGICRNRVTNNVKVYKLVANLPDYMITLKYVPG 60

DB 1 mktqtwiitciy1qlllfp1vktegicrnrvtnnvkdvtklvanlpkdymltklyvp 60

QY 61 MDVLPSCHWISEWVQVLSLTDLDKFSNISGSLNSYSLIDKLNVIVDDLYECKENSS 120
 DB 61 mdvlpshcwisewvq1dsdldldkfsniseglsnyslidlknv1vddlyecvkenss 120

QY 121 KDLKSKFSKSPERLFTPEEFIRLFRSIDAFKDFVASETSCVVSSTLSPEKDSRVSVT 180
 DB 121 KDLKSKFSKSPERLFTPEEFIRLFRSIDAFKDFVASETSCVVSSTLSPEKDSRVSVT 180

QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
 DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 11

AA011711
 ID AAR11711 standard; Protein: 273 AA.

AC AAR11711;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor from HT1080 fibrosarcoma line.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= sig_peptide

FT Protein 26..273 /label= mat_protein

EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-0505548.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

DR WPI: 1991-119233/17.

DR N-PSDB; AA011542.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have haematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

PS Disclosure; Fig 42; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AA011509-Q11543.

XX Sequence 273 AA;

SO

Query Match

Best local similarity 97.1%; Score 1030; DB 12; Length 273;

Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKTQWIIITCIYQLLEPNPLVKTEGICRNRYTNVNVKDYTLVNLPRKDYITLKYPG 60
DB 1 mkkctwlltcylqlllfnplvktegicrnrvtnnvkdvtklvankpdkymiltikypg 60
OY 61 MDVLPSCWISSEMVVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDIVECKENSS 120
DB 61 mdvlpshcwisemvqvlsdsltldkfsnlsesglsnysiidklvniyddiveckenss 120
OY 121 KDLKSEFSPEPRLTPEEFPRIRNRSIDAKDFVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 kdlkksfkspeprlftpeeffrfrlnrsidafkdfvasetsdcvvsstlspekdsrvsvt 180
OY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 kpfmlppvaasslrndssssnrk 203

RESULT 12

AAR20647
ID AAR20647 standard; Protein: 273 AA.

AC AAR20647;

DT 30-APR-1992 (first entry)

DE Human mast cell growth factor.

KW hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
proliferation.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..25 /label= signal

FT Region 26..210 /label= extracellular

FT /note= "claimed polypeptide"

FT Region 211..237 /label= transmembrane

FT Region 238..273 /label= intracellular

PN W09200376-A.

PD 09-JAN-1992.

FE 14-JUN-1991; 91WO-US04274.

XX 25-JUN-1990; 90US-0543264.

PR 10-AUG-1990; 90US-0565840.

PR 28-AUG-1990; 90US-0574152.

PR 21-SEP-1990; 90US-0586073.

PR 12-JUN-1991; 91US-0713715.

PA (IMMO-) IMMUNEX CORP.

XX Williams DE, Lyman S;

PI WPI; 1992-041558/05.

DR N-PSDB; AAQ20845.

XX New isolated DNA encoding human mast cell growth factor - useful in
PT stimulating proliferation of hematopoietic cells with growth factor,
PT to treat haemolytic and hypoproliferative anaemias
XX Claim 10; Fig 4; 59pp; English.
PS This human MGF has a mature extracellular region of 185 amino acids.
CC There is a second form of hMGF (see AAQ20844) resulting from an

CC alternative mRNA splicing event which deletes an exon encoding an
CC additional 28 amino acids beginning at amino acid 148 of the mature
CC protein. MGF is the ligand for the protein receptor expression product
CC of the c-kit proto-oncogene. MGF can be used to augment the
CC activity of other cytokines. It can influence early lymphoid or
CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
XX

SQ Sequence 273 AA;

Query Match 97.1%; Score 1030; DB 13; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKTQWIIITCIYQLLEPNPLVKTEGICRNRYTNVNVKDYTLVNLPRKDYITLKYPG 60
DB 1 mkkctwlltcylqlllfnplvktegicrnrvtnnvkdvtklvankpdkymiltikypg 60
OY 61 MDVLPSCWISSEMVVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDIVECKENSS 120
DB 61 mdvlpshcwisemvqvlsdsltldkfsnlsesglsnysiidklvniyddiveckenss 120
OY 121 KDLKSEFSPEPRLTPEEFPRIRNRSIDAKDFVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 kdlkksfkspeprlftpeeffrfrlnrsidafkdfvasetsdcvvsstlspekdsrvsvt 180
OY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 kpfmlppvaasslrndssssnrk 203

RESULT 13

AAR83978
ID AAR83978 standard; Protein: 273 AA.

AC AAR83978;

DT 15-MAY-1996 (first entry)

DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.

KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..25 /label= sig_peptide

FT Protein 26..248 /label= mat_SCF

PN EP676470-A1.

PD 11-OCT-1995.

FE 04-OCT-1990; 90EP-0105391.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

PA (AMGE-) AMGEN INC.

XX Boeselman RA, Martin FH, Suggs SV, Zsebo KW;

PI WPI; 1995-346090/45.

DR N-PSDB; AAT04890.

XX New stem cell factor polypeptide(s) - for stimulating the growth of

PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 PS Claim 9; Fig 42; 127pp; English.
 XX
 CC AAR83978 is a human stem cell factor (SCF) derived from the HT1080
 CC fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 XX
 SQ Sequence 273 AA;
 Query Match 97.1%; Score 1030; DB 16; Length 273;
 Best Local Similarity 99.5%; Pred. No. 1.1e-100;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCYIQLLLPLVKTGICRNRVNNVAVDKLVANLPKDYMTLKYPG 60
 Db 1 mkkqtwlltcylqlllfpvktgicrnrvnnvdklvaniipkdymltkypg 60
 QY 61 MDVLPSCWISEMWVQLSDSLTDLKFSNISEGNSYSLDKLVNIYVDLVECKENSS 120
 Db 61 mdvlpshcwisemvqlsdsldtlkfsniseglsnyldklnivldlveckenss 120
 QY 121 KDILKSFSPERLFTPEEFRIENRSIDAFKDVVASSETSDCVVSTLSPKDSRVSVT 180
 Db 121 kdilksfkspeprlftpeefrinfnsidafkdfvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFLPPVAASLRNDSSSSNSK 203
 Db 181 kpflppvaaslrndssssnsk 203
 RESULT 14
 AAM27607
 ID AAM27607 standard; Protein; 273 AA.
 XX
 AC AAM27607;
 XX
 DT 28-APR-1998 (first entry)
 XX
 DE Human recombinant stem cell factor protein.
 XX
 KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; SUF; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= leader sequence
 FT Protein 26..274
 FT /note= "mature full length stem cell factor protein"
 XX
 XX MO9738101-A1.
 XX
 XX 16-OCT-1997.
 PD
 XX
 PF 03-APR-1997; 97WO-US05541.

XX
 PR 05-APR-1996; 96US-0628428.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 PI Lu HS;
 XX
 DR WI; 1997-512718/47.
 XX
 PT Stem cell factor analogue N10D or N10D/N11D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder
 XX
 PS Claim 2; Fig 1; 42pp; English.
 XX
 CC This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SUF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAM27605 and AAM27606)
 CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used to treat pigmentation disorders, e.g.
 CC vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitise cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.
 XX
 SQ Sequence 273 AA;
 Query Match 97.1%; Score 1030; DB 18; Length 273;
 Best Local Similarity 99.5%; Pred. No. 1.1e-100;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCYIQLLLPLVKTGICRNRVNNVAVDKLVANLPKDYMTLKYPG 60
 Db 1 mkkqtwlltcylqlllfpvktgicrnrvnnvdklvaniipkdymltkypg 60
 QY 61 MDVLPSCWISEMWVQLSDSLTDLKFSNISEGNSYSLDKLVNIYVDLVECKENSS 120
 Db 61 mdvlpshcwisemvqlsdsldtlkfsniseglsnyldklnivldlveckenss 120
 QY 121 KDILKSFSPERLFTPEEFRIENRSIDAFKDVVASSETSDCVVSTLSPKDSRVSVT 180
 Db 121 kdilksfkspeprlftpeefrinfnsidafkdfvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFLPPVAASLRNDSSSSNSK 203
 Db 181 kpflppvaaslrndssssnsk 203
 RESULT 15
 AAY53284
 ID AAY53284 standard; Protein; 273 AA.
 XX
 AC AAY53284;
 XX
 DT 27-JUL-2000 (first entry)
 XX
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX
 KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; synergic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 KW cancer.
 XX
 OS Homo sapiens.

Search completed: August 18, 2002, 13:08:01
Job time: 406 sec

XX EP92579-A1.
PN
XX
PD 12-APR-2000.
XX
PF 04-OCT-1990; 99EP-0122861.
XX
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WD-0505548.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
XX
XX (AMGE-) AMGEN INC.
PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX
XX WPI: 2000-259135/23.
DR N-PSDB; AAA13714.
XX
XX Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor .
XX
PS Claim 22; Fig 42; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the
CC cells by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is
CC useful for expanding early haematopoietic progenitors in syngeneic,
CC allogeneic or autologous bone marrow transplant. SCF is useful for
CC enhancing the efficiency of gene therapy based on transfecting
CC haematopoietic stem cells. SCF is also useful for combating the
CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
CC haematopoietic recovery after acute blood loss and as a boost to the
CC immune system for fighting neoplasia (cancer). The present sequence
CC represents a specifically claimed human SCF from the present invention.
XX
SQ Sequence 273 AA;

Query Match 97.1%; Score 1030; DB 21; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWITITCTIYQLLFNPLVKTGICRNRVTNNVKDVTKLVAANLPKDYMITLKYVPG 60
DB 1 mktqtwiltctiyqlllfnplvktgicrnrvtnnvkdvtklvaanlpkdymitlkyvpg 60
QY 61 MDVPSHCWISBMVYQSLDLSLTLDFKFSITSEGLSNYSIIDKLNVYVDLVECKENSS 120
DB 61 mdvpschwisbmvyqslsdlsldlfkfsitseglsnysiidklvnvddlveckenass 120
QY 121 KDIKSEKSPPEPLFTPEPEFRINRSIDAKDFVASETSDCVVSSSTLSPEKDSRVSVT 180
DB 121 kdiksekspeplftpepefrinrsidakdfvasetsdcvssstlspekdsrvsvt 180
QY 181 KPFMLPVAASLRNDSSSSNSK 203
DB 181 kpfmlpvaaslrndssssnsk 203
DB 181 kpfmlpvaaslrndssssnsk 203

Sun Aug 18 14:09:01 2002

us-09-604-325a-46.rag

Page 11

4
1
1
1
1

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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 41.62 Seconds
(without alignments)
122.069 Million cell updates/sec

Title: US-09-604-325A-46

Perfect score: 1061

Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLRNDSNSSKYYILI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	208	4	US-08-836-252A-6
2	1061	100.0	208	4	US-08-482-918-46
3	1061	100.0	208	4	US-09-224-681-46
4	1061	100.0	208	4	US-08-336-728A-46
5	1030	97.1	273	1	US-08-220-379B-2
6	1030	97.1	273	2	US-08-628-428-9
7	1030	97.1	273	4	US-08-482-918-48
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9	1030	97.1	273	4	US-08-482-918-50
10	1030	97.1	273	4	US-09-224-681-48
11	1030	97.1	273	4	US-09-224-681-49
12	1030	97.1	273	4	US-09-224-681-50
13	1030	97.1	273	4	US-08-336-728A-48
14	1030	97.1	273	4	US-08-336-728A-49
15	1030	97.1	273	4	US-08-336-728A-50
16	1026	96.7	273	4	US-08-482-918-50
17	1026	96.7	273	4	US-09-224-681-50
18	1026	96.7	273	4	US-08-336-728A-50
19	1001	94.3	196	4	US-08-336-728A-44
20	975	91.9	424	5	PCT-US95-03866-14
21	974	91.8	424	5	PCT-US95-03866-12
22	920	86.7	266	4	US-08-482-918-57
23	920	86.7	266	4	US-09-224-681-57
24	920	86.7	266	4	US-08-336-728A-57
25	898	84.6	248	4	US-08-955-848A-82
26	897.5	84.6	274	4	US-08-336-728A-52
27	896.5	84.5	205	1	US-08-133-979A-4

28	896.5	84.5	205	2	US-08-436-890-4	Sequence 4, Appl
29	896.5	84.5	205	2	US-08-451-213-4	Sequence 4, Appl
30	890	83.9	245	4	US-08-482-918-63	Sequence 63, Appl
31	890	83.9	245	4	US-09-224-681-63	Sequence 63, Appl
32	890	83.9	245	4	US-08-336-728A-63	Sequence 63, Appl
33	884	83.3	271	4	US-08-482-918-52	Sequence 52, Appl
34	884	83.3	271	4	US-09-224-681-52	Sequence 52, Appl
35	880.5	83.0	274	4	US-08-336-728A-53	Sequence 53, Appl
36	875	82.5	273	4	US-08-482-918-53	Sequence 53, Appl
37	875	82.5	273	4	US-09-224-681-53	Sequence 53, Appl
38	865	81.5	195	4	US-08-482-918-44	Sequence 44, Appl
39	865	81.5	195	4	US-09-224-681-44	Sequence 44, Appl
40	862.5	81.3	274	4	US-08-482-918-51	Sequence 51, Appl
41	862.5	81.3	274	4	US-09-224-681-51	Sequence 51, Appl
42	862.5	81.3	274	4	US-08-336-728A-51	Sequence 51, Appl
43	861	81.1	273	4	US-08-482-918-42	Sequence 42, Appl
44	861	81.1	273	4	US-09-224-681-42	Sequence 42, Appl
45	861	81.1	273	4	US-08-336-728A-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-836-252A-6
Sequence 6, Application US/08836252A
Patent No. 6177556

GENERAL INFORMATION:

APPLICANT: Sharkey, Andrew M.
APPLICANT: Smith, Stephen K.
APPLICANT: Dellow, Kimberley A.
TITLE OF INVENTION: HUMAN SCF, A SPLICED VARIANT THEREOF, ITS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836, 252A
FILING DATE: 31-JULY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/GB95/02547
FILING DATE: 31-OCT-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422293.2
FILING DATE: 04-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9508618.7
FILING DATE: 28-APR-1995

ATTORNEY/AGENT INFORMATION:
NAME: ROBERT W. ESMOND
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0550000
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-836-252A-6

Query Match 100.0%; Score 1061; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLSHCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
DB 61 MDVLSHCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
QY 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKRYILI 208
DB 181 KPFLPVAASLRNDSSSNKRYILI 208

RESULT 2

US-08-482-918-46
; Sequence 46, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-46

Query Match 100.0%; Score 1061; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60

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DB 61 MDVLSHCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120

QY 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFLPVAASLRNDSSSNKRYILI 208
DB 181 KPFLPVAASLRNDSSSNKRYILI 208

RESULT 3

US-09-224-681-46
; Sequence 46, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/962,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
 TELEEX:
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-224-681-46

Query Match 100.0%; Score 1061; DB 4; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.3e-101;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVLTGICRNRYNNVNDVKLVANLPKDYMTLLKYPG 60
 DB 1 MKKTQWILTCIYLQLLFNPVLTGICRNRYNNVNDVKLVANLPKDYMTLLKYPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMYVQLSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFMLPPVAASLRNDSSSSNSKYIYL 208
 DB 181 KPFMLPPVAASLRNDSSSSNSKYIYL 208

RESULT 4
 US-08-336-728A-46
 Sequence 46, Application US/08336728A
 Patent No. 6207802
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Krisztina M.
 APPLICANT: Bosselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/336,728A
 FILING DATE: 09-NOV-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/588,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/32956
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEEX: 25-3856
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-336-728A-46

Query Match 100.0%; Score 1061; DB 4; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.3e-101;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVLTGICRNRYNNVNDVKLVANLPKDYMTLLKYPG 60
 DB 1 MKKTQWILTCIYLQLLFNPVLTGICRNRYNNVNDVKLVANLPKDYMTLLKYPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMYVQLSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFMLPPVAASLRNDSSSSNSKYIYL 208
 DB 181 KPFMLPPVAASLRNDSSSSNSKYIYL 208

RESULT 5
 US-08-220-379B-2
 Sequence 2, Application US/08220379B
 Patent No. 5525708
 GENERAL INFORMATION:
 APPLICANT: No. 5525708Ka, Karl
 APPLICANT: Lobell, Robert B
 TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/220,379B
 FILING DATE: 28-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr, James F
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: Cytomed/2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164...165
US-08-220-379B-2

Query Match 97.1% Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNVKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNVKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMVOQLSDLTDLDFKSNISEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISEMVOQLSDLTDLDFKSNISEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPPVAASLIRNDSSSNRK 203
DB 181 KPFMLPPVAASLIRNDSSSNRK 203

RESULT 6
US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962

GENERAL INFORMATION:

APPLICANT: Lu, Hsieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note="NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."

US-08-628-428-9

Query Match 97.1% Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNVKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNVKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMVOQLSDLTDLDFKSNISEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISEMVOQLSDLTDLDFKSNISEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPPVAASLIRNDSSSNRK 203
DB 181 KPFMLPPVAASLIRNDSSSNRK 203

RESULT 7
US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zsedo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1% Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNVKDYTKLVANLPKDYMITLKYVG 60

Db 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRTNNVKVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120
 Db 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPEMLPPVAASSLRNDSSSSNRK 203
 Db 181 KPEMLPPVAASSLRNDSSSSNRK 203

RESULT 8
 US-08-482-918-49
 : Sequence 49, Application US/08482918
 : Patent No. 6207417

GENERAL INFORMATION:
 : APPLICANT: Zsebo, Krisztina M.
 : APPLICANT: Bosselman, Robert A.
 : APPLICANT: Suggs, Sidney V.
 : APPLICANT: Martin, Francis H.
 : TITLE OF INVENTION: Stem Cell Factor
 : NUMBER OF SEQUENCES: 104
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 : STREET: 6300 Sears Tower, 233 South Wacker Drive
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: United States of America
 : ZIP: 60606-6402
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/482,918
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Clough, David W.
 : REGISTRATION NUMBER: 36,107
 : REFERENCE/DOCKET NUMBER: 01017/33005
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312/474-6300
 : TELEFAX: 312/474-0448
 : TELEX: 25-3856
 : INFORMATION FOR SEQ ID NO: 49:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 273 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-482-918-49

Query Match 97.1%; Score 1030; DB 4; Length 273;
 Best Local Similarity 99.5%; Pred. No. 3e-98;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRTNNVKVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRTNNVKVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120
 Db 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPEMLPPVAASSLRNDSSSSNRK 203
 Db 181 KPEMLPPVAASSLRNDSSSSNRK 203

RESULT 9
 US-08-482-918-61
 : Sequence 61, Application US/08482918
 : Patent No. 6207417

GENERAL INFORMATION:
 : APPLICANT: Zsebo, Krisztina M.
 : APPLICANT: Bosselman, Robert A.
 : APPLICANT: Suggs, Sidney V.
 : APPLICANT: Martin, Francis H.
 : TITLE OF INVENTION: Stem Cell Factor
 : NUMBER OF SEQUENCES: 104
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 : STREET: 6300 Sears Tower, 233 South Wacker Drive
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: United States of America
 : ZIP: 60606-6402
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/482,918
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Clough, David W.
 : REGISTRATION NUMBER: 36,107
 : REFERENCE/DOCKET NUMBER: 01017/33005
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312/474-6300
 : TELEFAX: 312/474-0448
 : TELEX: 25-3856
 : INFORMATION FOR SEQ ID NO: 61:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 273 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-482-918-61

Query Match 97.1%; Score 1030; DB 4; Length 273;
 Best Local Similarity 99.5%; Pred. No. 3e-98;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRTNNVKVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRTNNVKVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120
 Db 61 MDVLPSCWISSEWVYOLSLDLDKFSNISSEGLSNYSIIDKLVINVDLVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPEMLPPVAASSLRNDSSSSNRK 203
 Db 181 KPEMLPPVAASSLRNDSSSSNRK 203

RESULT 10
US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILCTCYLQLLFNPVLTGEGICRRNRYTNVKNVDYTKLVANLPKDMITLTKYVP 60
DB 1 MKKTQWILCTCYLQLLFNPVLTGEGICRRNRYTNVKNVDYTKLVANLPKDMITLTKYVP 60
QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISELSNYSIIDKLVINVDLVCEVKNSS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISELSNYSIIDKLVINVDLVCEVKNSS 120
QY 121 KDLKRSKSPPEPLFTEPEFRIRNRSIDAFKDPVVASSETPDCVSSSTLSPEKDSRYVT 180
DB 121 KDLKRSKSPPEPLFTEPEFRIRNRSIDAFKDPVVASSETPDCVSSSTLSPEKDSRYVT 180
QY 181 KPFMLPVAASSLRNDSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSNSK 203
RESULT 11
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQTWTWTCIYQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKQTWTWTCIYQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYDVLVECVKENS 120
QY 121 KDLKSEKSPPEPLPTPEEFPRIRNSIDAEPVAVASSTDCVVSSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPPEPLPTPEEFPRIRNSIDAEPVAVASSTDCVVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPPVAASSLRNDSSSSNSK 203

RESULT 12

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/962,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQTWTWTCIYQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKQTWTWTCIYQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYDVLVECVKENS 120
QY 121 KDLKSEKSPPEPLPTPEEFPRIRNSIDAEPVAVASSTDCVVSSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPPEPLPTPEEFPRIRNSIDAEPVAVASSTDCVVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPPVAASSLRNDSSSSNSK 203

RESULT 13

US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match          97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQILLFNPVLTGICRNRVTNNKVDYTKLVANLPKDYMITLKYVPG 60
Db 1 MKKTQWILTCIYQILLFNPVLTGICRNRVTNNKVDYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISEMNVQSLDSDLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
Db 61 MDVLPSCWISEMNVQSLDSDLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLSKFSKSPERLFTPEEFRIENRSIDAFKDPVVAASEISDCVASTLSPEKDSRVSVT 180
Db 121 KDLSKFSKSPERLFTPEEFRIENRSIDAFKDPVVAASEISDCVASTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNRK 203
Db 181 KPFMLPVAASSLRNDSSSSNRK 203

RESULT 14
US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
```

```

COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match          97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQILLFNPVLTGICRNRVTNNKVDYTKLVANLPKDYMITLKYVPG 60
Db 1 MKKTQWILTCIYQILLFNPVLTGICRNRVTNNKVDYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISEMNVQSLDSDLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
Db 61 MDVLPSCWISEMNVQSLDSDLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLSKFSKSPERLFTPEEFRIENRSIDAFKDPVVAASEISDCVASTLSPEKDSRVSVT 180
Db 121 KDLSKFSKSPERLFTPEEFRIENRSIDAFKDPVVAASEISDCVASTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNRK 203
Db 181 KPFMLPVAASSLRNDSSSSNRK 203

RESULT 15
US-08-336-728A-61
Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
```


Search completed: August 18, 2002, 13:04:01
Job time: 166 Sec

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYIQLLFNPLVKTREGICRNVTNNVKDVTKIVANLPKDMYITLTKYVG 60
DB 1 MKKTQWILTCIYIQLLFNPLVKTREGICRNVTNNVKDVTKIVANLPKDMYITLTKYVG 60
QY 61 MDVPSHCWISSEMYVQLSDSLDLDKFSNISSEGISNYSIDKLVNIYDDVLEVCYKENS 120
DB 61 MDVPSHCWISSEMYVQLSDSLDLDKFSNISSEGISNYSIDKLVNIYDDVLEVCYKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIFRNSIDAFKDYVASSETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIFRNSIDAFKDYVASSETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASLRNDSSSSNSK 203
DB 181 KPEMLPVAASLRNDSSSSNSK 203

Sun Aug 18 14:09:01 2002

us-09-604-325a-46.rai

Page 10

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 62.73 Seconds

(Without alignments)
318.613 Million cell updates/sec

Title: US-09-604-325a-46

Sequence: 1 MKKTQWILTCIYLQLLEN.....AASLRDSSSSSKYILI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	A35974	mast cell growth f
2	899.5	84.8	274	I46575	c-kit ligand - pig
3	890	83.9	245	B61190	mast cell growth f
4	886.5	83.6	274	S47571	stem cell factor
5	885.5	83.5	202	S58313	stem cell factor
6	862.5	81.3	274	I46929	stem cell factor
7	857	80.8	201	B35974	stem cell factor
8	855	80.6	273	S65801	stem cell factor
9	715	67.4	245	A37934	mast cell growth f
10	576.5	54.3	124	S29052	mast cell growth f
11	570.5	53.8	287	S70366	stem cell factor
12	562.5	53.0	287	JN0637	stem cell factor
13	479.5	45.2	253	S70367	stem cell factor
14	175.5	16.5	51	B35971	stem cell factor
15	172.5	16.3	49	A35971	stem cell growth f
16	97.5	9.2	1490	T16086	hypothetical prote
17	97	9.1	1447	F82909	hypothetical prote
18	94	8.9	1293	T27886	hypothetical prote
19	94	8.9	1813	T19295	hypothetical prote
20	92.5	8.7	164	B69616	cell-division init
21	92.5	8.7	512	G86773	clatrate (pro-35)-1
22	92	8.7	935	S63261	SEC21 protein - ye
23	91	8.6	1107	S61667	probable membrane
24	90.5	8.5	616	A69136	ATP-dependent GTP
25	89	8.4	1734	A41101	phorbol ester-bind
26	88.5	8.3	545	B44054	ort2 protein - Jun
27	88.5	8.3	941	B84855	phosphoenolpyruvat
28	88	8.3	335	S44922	k18 antigen - Enta
29	88	8.3	465	H97165	flagellar hook-len

30	88	8.3	702	F97352	membrane-associate
31	88	8.3	1690	T31670	DNA-directed RNA p
32	87.5	8.2	649	T04005	probable protein k
33	87.5	8.2	966	S26235	phosphoenolpyruvat
34	87	8.2	664	T16411	hypothetical prote
35	86.5	8.2	246	T19850	hypothetical prote
36	86.5	8.2	436	F86486	hypothetical prote
37	86.5	8.2	844	S61104	protein F28J9.3 (1
38	86.5	8.2	1271	T08607	BRO1 protein - yea
39	86	8.1	246	A64579	hypothetical prote
40	86	8.1	496	G86887	molybdenum ABC tra
41	86	8.1	660	T23794	theonine synthase
42	86	8.1	1334	T18493	hypothetical prote
43	85.5	8.1	222	T23762	hypothetical prote
44	85.5	8.1	614	B86461	probable protein k
45	85.5	8.1	636	A45949	merozoite surface

ALIGNMENTS

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RESULT 1
A35974
M:Alternate names: Kit ligand, stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35974, A61190
R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris,
S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell facto
A:Reference number: A35974; MUID:91004219
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M5964; NID:q337933; PIDN:AAA8450.1; PID:q337934
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro
Cell Growth Differ. 2: 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and local
A:Reference number: A61190; MUID:92172791
A:Accession: A61190
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Genetics:
A:Gene: GDB:MGR
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-273/Product: mast cell growth factor #status predicted <MCS>
F:26-188/Product: (or 26-190) mast cell growth factor, soluble form #status predicted
F:215-237/Domain: transmembrane #status predicted <TM>
F:90,97,118,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          97.1%  Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%  Pred. No. 3.7e-75;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MKKTQWILTCIYLQLLENFNLVTEGICRNRYNNKVDYTKLVANLPKDYMITLKYVP 60

Db 1 MKKTQWILTCIYLQLLENFNLVTEGICRNRYNNKVDYTKLVANLPKDYMITLKYVP 60

QY 61 MDVPSHCWISSEMYVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKNSS 120

QY 61 MDVPSHCWISSEMYVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKNSS 120

Db 61 MDVPSHCWISSEMYVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKNSS 120

QY 121 KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVVAASESDCVSSTLSPKDSVSVY 180

QY 121 KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVVAASESDCVSSTLSPKDSVSVY 180

Db 121 KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVVAASESDCVSSTLSPKDSVSVY 180

Qy 181 KPFLPVAASSLRNDSSSSNSK 203
 Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 2
 146575
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 146575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: 146575; MUID:94146218
 A:Accession: 146575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <2HA>
 A:Cross-references: GB:L07786; NID:g164420; PIDN:AAA53670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 899.5; DB 2; Length 274;
 Best Local Similarity 86.3%; Pred. No. 1e-64;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Qy 121 KDKKSFSPSPRLFTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPKDSRVSV 179
 Db 121 ENVKSSKSPSPRLFTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPKDSRVSV 180
 Qy 180 TKPFMLPVAASSLRNDSSSSNSK 203
 Db 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 3
 B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localized
 A:Reference number: A61190; MUID:92172791
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage
 C:Genetics:
 A:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:90,97,118,145/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 83.9%; Score 890; DB 2; Length 245;

Best Local Similarity 100.0%; Pred. No. 5.1e-64;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Qy 121 KDKKSFSPSPRLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPK 173
 Db 121 KDKKSFSPSPRLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPK 173

RESULT 4
 S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine
 A:Reference number: S47571; MUID:94339176
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <2HO>
 A:Cross-references: EMBL:D28934; NID:g538520; PIDN:BA006061.1; PID:g538521
 C:Superfamily: mouse mast cell growth factor

Query Match 83.6%; Score 886.5; DB 2; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.1e-63;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Qy 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITTCIYQLLFLNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
 Qy 121 KDKKSFSPSPRLFTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPKDSRVSV 179
 Db 121 ENVKSSKSPSPRLFTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPKDSRVSV 180
 Qy 180 TKPFMLPVAASSLRNDSSSSNSK 203
 Db 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 5
 S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:g940807; PIDN:CAA90620.1; PID:g940808
 C:Superfamily: mouse mast cell growth factor

Query Match 83.5%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 9.2e-64;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60

QY 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120
 DB 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120

QY 121 KDLKSKSPERPLFTPEEFERIFNRSIDAFKDF-VVASETSDCVVSSITLSPKDSRVSV 179
 DB 121 ENVKAKRSPELRTPEEFERIFNRSIDAFKDFLETVASKSBCVVSITLSPKDSRVSV 180

QY 180 TKPFMLPPVAASSLRNDSSSSNGK 203
 DB 181 TKPFMLPPVAASSLRNDSSSSNGK 204

RESULT 7
 B35974
 stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, H.
 A:Title: Primary structure and functional expression of rat and human stem cell factor
 A:Reference number: A35974; MUID:91004219
 A:Accession: B35974
 A:Status: preliminary

Query Match 81.3%; Score 862.5; DB 2; Length 274;
 Best Local Similarity 84.8%; Pred. No. 9.4e-62;
 Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60

QY 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120
 DB 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120

QY 121 KDLKSKSPERPLFTPEEFERIFNRSIDAFKDF-VVASETSDCVVSSITLSPKDSRVSV 179
 DB 121 ENVKAKRSPELRTPEEFERIFNRSIDAFKDFLETVASKSBCVVSITLSPKDSRVSV 180

QY 180 TKPFMLPPVAASSLRNDSSSSNGK 203
 DB 181 TKPFMLPPVAASSLRNDSSSSNGK 204

RESULT 7
 B35974
 stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, H.
 A:Title: Primary structure and functional expression of rat and human stem cell factor
 A:Reference number: A35974; MUID:91004219
 A:Accession: B35974
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:g554507
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zse
 J. Biol. Chem. 266: 8102-8107, 1991
 A:Title: Amino acid sequence and post-translational modification of stem cell factor
 A:Reference number: A39805; MUID:91217037
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 7E/27-190 <LUA>
 C:Superfamily: mouse mast cell growth factor

Query Match 80.8%; Score 857; DB 2; Length 201;
 Best Local Similarity 82.6%; Pred. No. 1.7e-61;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWITTCIYQLLEFNPVLTKEGICRNRYNNKVDYTKLVANLPKDYMITLKYPVG 60

QY 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120
 DB 61 MDVLPSCWISIMVWVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINVDIVLVECKENSS 120

QY 121 KDLKSKSPERPLFTPEEFERIFNRSIDAFKDFVVAASETSDCVVSSITLSPKDSRVSV 180
 DB 121 KNVSELEKPEPRNFTPEEFERIFNRSIDAFKDFVVAASETSDCVVSSITLSPKDSRVSV 180

QY 181 KPFPMLPPVAASSLRNDSSSSN 201
 DB 181 KPFPMLPPVAASSLRNDSSSSN 201

RESULT 8
 S65801
 mast cell growth factor - mouse
 N:Alternate names: hematopoietic growth factor K1; ligand steel factor; stem cell fac
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
 C:Accession: S65801; A43751; A35976; A35977; A35972; A35975; A35973; I48768
 R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996
 A:Title: Multiple pathways for steel regulation suggested by genomic and sequence ana
 A:Reference number: S65801; MUID:97002351
 A:Accession: S65801
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <BED>
 A:Cross-references: EMBL:U44725; NID:g1172215; PIDN:AA052447.1; PID:g1172216
 M: Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the k
 A:Reference number: A43751; MUID:92330001
 A:Accession: A43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-214, 'U', 216-273 <HUA>
 A:Cross-references: GB:S40364; NID:9251668; PIDN:AA022554.2; PID:g5705957
 A:Note: The authors translated the codon TTG for residue 215 as Trp
 R:Huang, E.; Nocka, K.; Belter, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Le
 Cell 63, 225-233, 1990
 A:Title: The hematopoietic growth factor K1 is encoded by the Sl locus and is the lig
 A:Reference number: A35976; MUID:91004221
 A:Accession: A35976
 A:Status: preliminary
 A:Molecule type: not compared with conceptual translation
 A:Residues: 1-206, 'S', 208-270 <H02>
 A:Cross-references: GB:M38511
 R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; Mar
 Cell 63, 235-243, 1990
 A:Title: Molecular cloning of mast cell growth factor, a hematopoietic that is active

A:Reference number: A35977; MUID:91004223
 A:Accession: A35977
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <AND>
 A:Cross-references: GB:M57647; GB:M38436; NID:9199151; PIDN:AAA39538.1; PID:9199152
 R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; An
 Cell 63, 175-183, 1990
 A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
 A:Reference number: A35972; MUID:91004216
 A:Accession: A35972
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 26-53 <COP>
 A:Cross-references: GB:M59912
 R:Zebo, K.M.; Williams, D.A.; Geissler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.L.;
 ; Cattaneach, B.M.; Galli, S.J.; Suggs, S.V.
 Cell 63, 213-224, 1990
 A:Title: Stem cell factor is encoded at the sl locus of the mouse and is the ligand for
 A:Reference number: A35975; MUID:91004220
 A:Accession: A35975
 A:Molecule type: mRNA
 A:Residues: 1-201 <ZSE>
 A:Cross-references: GB:M59915; NID:9200935; PIDN:AAA40095.1; PID:9554271
 R:Zebo, K.M.; Wypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
 A.; Langley, K.E.
 Cell 63, 195-201, 1990
 A:Title: Identification, purification, and biological characterization of hematopoietic
 A:Reference number: A35973; MUID:91004218
 A:Accession: A35973
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-29, 'R', 31-39 <ZS2>
 R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
 Genes Dev. 6, 1832-1842, 1992
 A:Title: Developmental abnormalities in Steel17h mice result from a splicing defect in t
 A:Reference number: A44071; MUID:93012940
 A:Accession: 148768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', 208-273 <RES>
 A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA8778.1; PID:9395284
 C:Genetics:
 A:Gene: SLF
 A:Map position: 10
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 80.6%; Score 855; DB 2; Length 273;
 Best Local Similarity 82.3%; Pred. No. 3,7e-61;
 Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLOLLFNPLVTEGICRNRTNNVKNVDTKLVANLPKDYMITLKYPG 60
 |||||
 DB 1 MKKTQWITLCIYLOLLFNPLVTEGICRNRTNNVKNVDTKLVANLPKDYMITLKYPG 60
 |||||
 QY 61 MDVLPSCWISSENVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDLVECKENSS 120
 |||||
 DB 61 MDVLPSCWISSENVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDLVECKENAP 120
 |||||
 QY 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVASETSQCVSSSTSPKDSRVST 180
 |||||
 DB 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVASETSQCVSSSTSPKDSRVST 180
 |||||
 QY 181 KPMLPVAASLRNDSSSSNSK 203
 |||||
 DB 181 KPMLPVAASLRNDSSSSNSK 203
 |||||
 RESULT 9
 A37934
 mast cell growth factor precursor (version 2) - mouse

N:Alternate names: KL-2 protein
 C:Species: Mus musculus (house mouse)
 C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
 C:Accession: A37934; B43751
 R:Flanagan, J.G.; Chan, D.C.; Leder, P.
 Cell 64, 1025-1035, 1991
 A:Title: Transmembrane form of the kit ligand growth factor is determined by alternat
 A:Reference number: A37934; MUID:91160046
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <PLA>
 A:Cross-references: GB:M64262
 R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the k
 A:Reference number: A43751; MUID:92330001
 A:Accession: B43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

Query Match 67.4%; Score 715; DB 2; Length 245;
 Best Local Similarity 79.8%; Pred. No. 5.2e-50;
 Matches 138; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLOLLFNPLVTEGICRNRTNNVKNVDTKLVANLPKDYMITLKYPG 60
 |||||
 DB 1 MKKTQWITLCIYLOLLFNPLVTEGICRNRTNNVKNVDTKLVANLPKDYMITLKYPG 60
 |||||
 QY 61 MDVLPSCWISSENVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDLVECKENSS 120
 |||||
 DB 61 MDVLPSCWISSENVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDLVECKENAP 120
 |||||
 QY 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVASETSQCVSSSTSPKDSRVST 173
 |||||
 DB 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVASETSQCVSSSTSPKDSRVST 173
 |||||
 RESULT 10
 S29052
 Stem cell factor - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S29052
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Balter
 Arch. Biochem. Biophys. 298, 150-158, 1992
 A:Title: Post-translational processing of membrane-associated recombinant human stem
 A:Reference number: S29052; MUID:92398336
 A:Accession: S29052
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-113; 14-30; 31-46; 47-59; 60-86; 87-95; 96-107; 108-124 <LUB>
 C:Superfamily: mouse mast cell growth factor

Query Match 54.3%; Score 576.5; DB 2; Length 124;
 Best Local Similarity 75.2%; Pred. No. 2.7e-39;
 Matches 124; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

QY 26 EGICRNRTNNVKNVDTKLVANLPKDYMITLKYPGCMVLPSCWISSENVQVLSLTL 85
 |||||
 DB 1 EGICRNRTNNVKNVDTKLVANLPKDYMITLKYPGCMVLPSCWISSENVQVLSLTL 85
 |||||
 QY 86 DKFSNISGLSNYSIIDKLVINIVDLVECKENSSKDLKSKFSPEPLFTPEEFRIFN 145
 |||||
 DB 31 DKFSNISGLSNYSIIDKLVINIVDLVECKENSSKDLKSKFSPEPLFTPEEFRIFN 83
 |||||
 QY 146 RSIDAFKDFVASETSQCVSSSTSPKDSRVSTKPMLPVA 190

Db 84 RSI----DFVASETSDCVSSSTLSPEKDSRVSVTKPFMLPVA 124

```

RESULT 11
S70366
stem cell factor long form precursor - quail
C:Species: Columba columba (quail)
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70366
R:Petitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell factor
A:Reference number: S70366; MUID:96283808
A:Accession: S70366
A:Molecule type: mRNA
A:Residues: 1-287 <PEPT>
A:Cross-references: EMBL:U043078; NID:g1150875; PIDN:AAC59933.1; PID:g1150876
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-287/Product: stem cell factor long form #status predicted <MAT>
F:226-250/Domain: transmembrane #status predicted <TM>

```

Query Match	53.8%;	Score 570.5;	DB 2;	Length 287;
Best Local Similarity	55.1%;	Pred. No. 2.4e-38;		
Matches 114;	Conservative 37;	Mismatches 51;	Indels 5;	Gaps 3;

```

QY      1 MKKQTMATLTCITAYKÖLLLENPLVTEBICGNRVYNNKVDYTKVLVANI.KRYMATTTKVPG 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 MKKQTMATITTCFCLQÖLLLENPLVATQSSCGNAPYTDVNDIAKLGNLPNDYLTTLKRVPK 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 MDVLPBHCWISERNVQVLSLTDLIDLDFK--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61 MDSLPHNCHLWMPBESRSRLAHNLTQKFVDYISDMSPVLSNYSIIINNLTRIINDIMACLAF 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      118 NSSKD-LKSEFKSEPEPLTFPEEFERFIENRSDAFKDEYVAASETSDCVYSSTL-SEPKS 175
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 DKNDPDFIKENGHLYEEDREFIPENEFRLFNRTIEYKEFAUSDLDKNDQIMPSYETEPENDS 180
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      176 RVSYTKPFMLPVAASSLRLDSSSSNS 202
        ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      181 RVAATKTIISFPVAASSLRLDSSIGSNT 207
        ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12

JN0637

stem cell factor precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000

C:Accession: JN0637

R:Zhou, J.H.; Ohkaki, M.; Sakurai, M.

Gene 127, 269-270, 1993

A:Title: Sequence of a cDNA encoding chicken stem cell factor.

A:Reference number: JN0637; MUID:93273244

A:Accession: JN0637

A:Molecule type: mRNA

A:Residues: 1-287 <ZHO>

A:Cross-references: GB:D13516; NID:g9391648; PIDN:BAAO2733.1; PID:g9391649

A:Experimental source: brain

C:Superfamily: mouse mast cell growth factor

C:Keywords: growth factor; transmembrane protein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-287/Product: stem cell factor #status predicted <MAT>

F:226-248/Domain: transmembrane #status predicted <TM>

Query Match	53.0%;	Score 562.5;	DB 2;	Length 287;
Best Local Similarity	54.6%;	Pred. No. 1e-37;		
Matches 113;	Conservative 36;	Mismatches 53;	Indels 5;	Gaps 3;

```

Db      1 MKKQQTWITITFCQLLLILNLPVKAQSSCCGNPVPDGVNDVIAKLGVNLPENDYLLTLIKVYPK 60
Qy      61 MDVAIPSHQWISSEMYVOLSDSLTDILDDKFSNT---SELSWYSTIDKLVNIVDDVLECAYKE 117
Db      61 MDSLPNHCWILAMPPEFSRSJLHNLFQKFSQSDSDMSDVLSWYSTINLTTRIINDIMACIAP 120
Qy      118 NSSKD-LKSKSESEPRLFTPEEFERFLFNKSIDAFKQFVVAASETSDCVVSSLT-SEKDS 175
Db      121 DKNKDFIKENGLIYEEDRFPIPENFERFLNSTIEVYKFAQSLDKNCKIMSTVETENDS 180
Qy      176 RVSATKPPMLDPVAASLRDSSSNS 202
Db      181 RVAATKTIISPPVAASLRDSSGNT 207

```

```

RESULT      13
S70367
stem cell factor short form precursor - qual1
C:Species: Coturnix coturnix (qual1)
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70367
R:Petitite, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell
A:Reference number: S70366; M0ID:96283808
A:Accession: S70367
A:Molecule type: mRNA
A:Residues: 1-253 <PEP>
A:Cross-references: EMBL:U43079; NID:g1150877; PIDN:MAC59934.1; PID:g1150878
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-253/Domain: signal sequence #status predicted <SIG>
F:26-253/Product: stem cell factor short form #status predicted <MAT>
F:192-216/Domain: transmembrane #status predicted <TM>

```

Query Match	45.2%;	Score 479.5;	DB 2;	Length 253;
Best Local Similarity	46.9%;	Pred. No. 3.9e-31;		
Matches 100; Conservative	42;	Mismatches 58;	Indels 13;	Gaps 4;

[illegible]

QY 176 RVSVTKPEMLPPVAASSLRNDSSSSNSKYYILI 208
 :::|::|::|
Dp 181 ALGF-----ISSSLGIGISALTSLSLILI 205

RESULT 14
B35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; W0ID:91004215
A:Accession: B35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-51 <WIL>
A:Superfamily: mouse mast cell growth factor

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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 35.93 Seconds
(Without alignments) 224.149 Million cell updates/sec

Title: US-09-604-325a-46
Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLRNDSNSSKXIIYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	97.1	273	1	SCF_HUMAN
2	899.5	84.8	274	1	SCF_PIG
3	862.5	81.3	274	1	SCF_CANFA
4	857	80.8	201	1	SCF_RAT
5	855	80.6	273	1	SCF_MOUSE
6	562.5	53.0	287	1	SCF_CHICK
7	102	9.6	981	1	SCA4_RICAR
8	92	8.7	935	1	COG_YEAST
9	90.5	8.5	1742	1	MYSC_HUMAN
10	89	8.4	989	1	PRP3_DICDI
11	89	8.4	1815	1	UN13_CAEEL
12	88.5	8.3	545	1	VNCS_JCDNY
13	87.5	8.2	664	1	CAPP_MEDSA
14	87	8.2	664	1	2AAA_CAEEL
15	86.5	8.2	644	1	BRO1_YEAST
16	84.5	8.0	466	1	DNAA_PROMT
17	84.5	8.0	964	1	CAPP_TOBAC
18	84.5	8.0	998	1	SCA4_RICAR
19	82.5	7.8	451	1	DNAA_PASMU
20	82.5	7.8	991	1	SCA4_RICAR
21	82	7.7	1140	1	YMG6_YEAST
22	82	7.7	1188	1	PEPA_METUA
23	82	7.7	1224	1	MSW1_YEAST
24	81	7.6	196	1	KITH_ASSEF
25	81	7.6	388	1	YAS5_METUA
26	81	7.6	490	1	CPOK_MACRA
27	80.5	7.6	373	1	BIOF_HELPJ
28	80.5	7.6	442	1	YUBI_ECOLI
29	80.5	7.6	755	1	P100_HSVJ7
30	80.5	7.6	2238	1	RRLI_BUNYW
31	80.5	7.6	4563	1	APB_HUMAN
32	80	7.5	480	1	YB9Q_YEAST
33	80	7.5	490	1	CPC8_HUMAN

34	79.5	7.5	447	1	DNAA_SYNY3	P49995 synecocyst
35	79.5	7.5	455	1	DNAA_LACIA	Q9CJ12 lactococcus
36	79.5	7.5	540	1	AXR1_ARATH	P42744 arabidopsis
37	79.5	7.5	640	1	UL06_HSVJ7	P52455 human herpes
38	79.5	7.5	729	1	CUR6_CAEEL	Q21346 caenorhabdi
39	79.5	7.5	737	1	SUV3_YEAST	P32580 saccharomyc
40	79.5	7.5	966	1	CAP1_MESCR	P10490 mesembryant
41	79.5	7.5	1294	1	YASB_SCHPO	Q09716 schizosacch
42	79	7.4	420	1	YMS7_YEAST	Q03694 saccharomyc
43	79	7.4	2492	1	TALA_DICDI	P54633 dictyosteli
44	78.5	7.4	166	1	INC_MARMO	Q35735 marmota mon
45	78.5	7.4	229	1	YSV4_CAEEL	Q10010 caenorhabdi

ALIGNMENTS

RESULT	1	STANDARD	PRT	273 AA
ID	SCF_HUMAN			
AC	P21583			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR MGF OR SCF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
ON	NCBI_TaxID=9606;			
OR	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91004219; Pubmed=2208279;			
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,			
RA	Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,			
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,			
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sacdev R.K.,			
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;			
RT	"Primary structure and functional expression of rat and human stem cell factor DNAs."			
RL	Cell 63:203-211(1990).			
CC	-!- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.			
CC	-!- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.			
CC	-!- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.			
CC	-!- SIMILARITY: BELONGS TO THE SCF FAMILY.			
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CC	EMBL: M59964; AAA85450.1; -.			
DR	PIR: A35974; A35974.			
DR	MIM: 184745; -.			
DR	InterPro: IPR003452; SCF.			
DR	Pfam: PF02404; SCF.1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.			
FT	SIGNAL	1	25	
FT	CHAIN	26	273	
FT	DOMAIN	26	214	
FT	TRANSMEM	215	237	
FT	DOMAIN	238	273	
FT	DISULFID	29	114	
FT	KIT LIGAND. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). BY SIMILARITY.			

FT DISULFID 68 163 BY SIMILARITY
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB596607 CRC64;

Query Match 97.1%; Score 1030; DB 1; Length 273;
 Best Local Similarity 99.5%; Pred. No. 1.4e-73;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPVLTGICRNRVTNNVADVKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWILTCIYQLLLFNPVLTGICRNRVTNNVADVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISBMVQVLSLTDLDKFSNISGLSNYSIIDKLVIYDDLYEVCENSS 120
 DB 61 MDVLPSCWISBMVQVLSLTDLDKFSNISGLSNYSIIDKLVIYDDLYEVCENSS 120
 QY 121 KDLKSKSPSPRLTPEEFERIFNRSIDAEKDVVASSETDCVVSSTLSPKDSRVSVT 180
 DB 121 KDLKSKSPSPRLTPEEFERIFNRSIDAEKDVVASSETDCVVSSTLSPKDSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSSNRK 203
 DB 181 KPFMLPPVAASSLRNDSSSSNRK 203

RESULT 2
 SCF_PIG STANDARD; PRT; 274 AA.
 AC 029030;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;
 RC MEDLINE=94146218; PubMed=7508758;
 RA Zhang Z., Anthony R.V.;
 RT "Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";
 RT Biol. Reprod. 50:95-102(1994).
 RL 1

-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS (BY SIMILARITY).
 -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
 -1- SIMILARITY: BELONGS TO THE SCF FAMILY.

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 CC
 CC EMBU: L07786; AAA53670.1; -
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF; 1.
 DR

KW Growth factor: Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT CHAIN 26 274 KIT LIGAND.
 FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 216 238 POTENTIAL.
 FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 29 114 BY SIMILARITY.
 FT DISULFID 68 164 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 274 AA; 31118 MW; FFC87114D7BA6A6 CRC64;

Query Match 84.8%; Score 899.5; DB 1; Length 274;
 Best Local Similarity 86.3%; Pred. No. 2.1e-63;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGICRNRVTNNVADVKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWILTCIYQLLLFNPVLTGICRNRVTNNVADVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISBMVQVLSLTDLDKFSNISGLSNYSIIDKLVIYDDLYEVCENSS 120
 DB 61 MDVLPSCWISBMVQVLSLTDLDKFSNISGLSNYSIIDKLVIYDDLYEVCENSS 120
 QY 121 KDLKSKSPSPRLTPEEFERIFNRSIDAEKDVVASSETDCVVSSTLSPKDSRVSVT 179
 DB 121 ENAKSKSPSPRLTPEEFERIFNRSIDAEKDVVASSETDCVVSSTLSPKDSRVSVT 180
 QY 180 TKPFMLPPVAASSLRNDSSSSNRK 203
 DB 181 TKPFMLPPVAASSLRNDSSSSNRK 204

RESULT 3
 SCF_CANFA STANDARD; PRT; 274 AA.
 AC 006220;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RC MEDLINE=93106145; PubMed=1281786;
 RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W., Martin F.H.;
 RT "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture.";
 RT Exp. Hematol. 20:1118-1124(1992).
 RL 1

-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
 -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
 -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 -1- SIMILARITY: BELONGS TO THE SCF FAMILY.

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 CC
 CC EMBU: L07786; AAA53670.1; -
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF; 1.
 DR

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DR EMBL: S53329; AAB24619.1; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.

KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT CARBOHYD 68 164
FT CARBOHYD 90 90
FT CARBOHYD 97 97
FT CARBOHYD 145 145
FT CARBOHYD 196 196
SQ SEQUENCE 274 AA; 30869 MW; 4182BE9AED00793B CRC64;

Query Match 81.3%; Score 862.5; DB 1; Length 274;
Best Local Similarity 84.8%; Pred. No. 1.6e-60;
Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQWILTCYIQLLLFNPLVKTGEGICRNVTNNKDVTKLVANLPKDWITLKYVPG 60
DB 1 MKKTQWITTCYIQLLLFNPLVKTGEGICRNVTNNKDVTKLVANLPKDWITLKYVPG 60

QY 61 MVLPSHCWISWVQVQSLDLDKFSNISSEGSNTSIIDKLVNIVDDIVECKENSS 120
DB 61 MVLPSHCWISWVQVQSLDLDKFSNISSEGSNTSIIDKLVNIVDDIVECKENSS 120
QY 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDF-VVASESDCVVSTLSPKDSRVSV 179
DB 121 EVVKKAPSPSELRLTPEEPFRIFNRSIDAFKDFVASKSECVVSTLSPKDSRVSV 180

QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 4
SCF_RAT STANDARD; PRT; 201 AA.
AC P21581;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF) (Fragment).
GN KITLG OR MGF.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RA Martin F.H., Sugis S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
RA Morris C.F., McInce I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
RA Fisher E.F., Ertel H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs."
RL Cell 63:203-211(1990).

RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RC STAIN-BUFFALO; TISSUE-Liver;
RX MEDLINE=91217037; Pubmed=1708771;

RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
RT "Amino acid sequence and post-translational modification of stem cell
RT factor isolated from buffalo rat liver cell-conditioned medium."
RL J. Biol. Chem. 266:8102-8107(1991).

RP SEQUENCE OF 26-39.
RX MEDLINE=91004218; Pubmed=2208278;
RA Zsebo K.M., Wypych J., McInce I.K., Lu H.S., Smith K.A.,
RA Karkare S.B., Sachdev R.K., Yushchenko V.N., Birkett N.C.,
RA Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz E.A.,
RA Langley K.E.;
RT "Identification, purification, and biological characterization of
RT hematopoietic stem cell factor from buffalo rat liver conditioned
RT medium."
RL Cell 63:195-201(1990).

CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
CC PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.

CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sdb.ch).

DR EMBL: M59966; AAA42117.1; -
DR PIR: B35974; B35974.
DR PIR: A35973; A35973.
DR InterPro: IPR003452; SCF.

DR Pfam: PF02404; SCF. 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 >201
FT MOD.RES 26 26
FT DISULFID 29 114
FT DISULFID 68 163
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 167 167
FT CARBOHYD 168 168
FT CARBOHYD 180 180
FT CARBOHYD 195 195
FT NON_TER 201 201

SO SEQUENCE 201 AA; 22537 MW; 188868C1DA4F271B CRC64;
KIT LIGAND.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .) (PARTIAL).
O-LINKED (PROBABLE).
O-LINKED (PROBABLE).
O-LINKED (PROBABLE).
N-LINKED (GLCNAC. . .) (PARTIAL).

Query Match 80.8%; Score 857; DB 1; Length 201;
Best Local Similarity 82.6%; Pred. No. 3e-60;
Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIQLLLFNPLVKTGEGICRNVTNNKDVTKLVANLPKDWITLKYVPG 60
DB 1 MKKTQWITTCYIQLLLFNPLVKTGEGICRNVTNNKDVTKLVANLPKDWITLKYVPG 60

QY 61 MVLPSHCWISWVQVQSLDLDKFSNISSEGSNTSIIDKLVNIVDDIVECKENSS 120
DB 61 MVLPSHCWISWVQVQSLDLDKFSNISSEGSNTSIIDKLVNIVDDIVECKENSS 120

QY 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVAVASESDCVVSTLSPKDSRVSV 180
DB 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVAVASESDCVVSTLSPKDSRVSV 180

QY 181 KPFMLPVAASSLRNDSSSSNSK 201
DB 181 KPFMLPVAASSLRNDSSSSNSK 201

DB 181 KPEMLPVAASLRNDSSSN 201

RESULT 5
SCF_MOUSE STANDARD: PRT: 273 AA.

AC 20826:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL) (KL-1 protein) (Steel factor).
GN KITLG OR KITL OR MGF OR SL OR SLF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCB6F1;
RA MEDLINE=91004223; PubMed=1698558;
RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
RA "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
RL Cell 63:235-243(1990).
RN

[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck K.J., Besmer P.;
RT "Differential expression and processing of two cell associated forms of the Kit-ligand: KL-1 and KL-2.";
RL Mol. Biol. Cell 3:349-362(1992).
RN

[3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=MCB6F1;
RA MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the Kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant.";
RL Cell 64:1025-1035(1991).
RN

[4]
RP SEQUENCE FROM N.A.
RA MEDLINE=93012940; PubMed=1383087;
RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A., Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
RT "Developmental abnormalities in Steel17H mice result from a splicing defect in the steel factor cytoplasmic tail.";
RL Genes Dev. 6:1832-1842(1992).
RN

[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=97002551; PubMed=8849898;
RA Bedell M.A., Copeland N.G., Jenkins N.A.;
RT "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene.";
RL Genetics 142:927-934(1996).
RN

[6]
RP SEQUENCE FROM N.A.
RC STRAIN=(102/ELXC3H/EL)F1; TISSUE=Brain;
RA Graw J.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN

[7]
RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
RA MEDLINE=91004221; PubMed=1698557;
RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck K.J., Lahm H.W., Wellner D., Leder P., Besmer P.;
RT "The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
RL Cell 63:225-233(1990).

[8]
RP SEQUENCE OF 1-201 FROM N.A.
RA MEDLINE=91004220; PubMed=1698556;
RA Zeebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murrack D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeshi T., Catnach B.M., Galli S.J., Sugas S.V.;
RT "Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for the c-kit tyrosine kinase receptor.";
RL Cell 63:213-224(1990).
RN

[9]
RP SEQUENCE OF 26-53.
RA MEDLINE=91004216; PubMed=1698554;
RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A., Cosman D., Anderson D., Lyman S.D., Williams D.E.;
RT "Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is deleted in a number of steel alleles.";
RL Cell 63:175-183(1990).
RN

[10]
RP PARTIAL SEQUENCE OF 26-78.
RA MEDLINE=91004215; PubMed=1698553;
RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.;
RT "Identification of a ligand for the c-kit proto-oncogene.";
RL Cell 63:167-174(1990).
RN

-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
CC
-1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
CC
-1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN VARYING RATIOS IN DIFFERENT TISSUES.
CC
-1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC
-1- PIM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
CC
-1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC

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CC
EMBL; M59915; AAA40095.1; -;
DR EMBL; M57647; AAA39538.1; -;
DR EMBL; X68989; CAA48778.1; -;
DR EMBL; U44724; -; NOT ANNOTATED_CDS.
DR EMBL; U44725; AAC52447.1; -;
DR EMBL; X9581; CAA64867.1; -;
DR EMBL; S40364; AAB22554.2; -;
DR EMBL; M59912; AAA39539.1; -;
DR PIR; A35971; A35971.
DR PIR; A35972; A35972.
DR PIR; A35975; A35975.
DR PIR; A35976; A35976.
DR PIR; A35977; A35977.
DR PIR; A43751; A43751.
DR PIR; B35971; B35971.
DR MGI; MGI:96974; Kitl.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal;
KW Alternative splicing; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 273 KIT LIGAND.

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FT DOMAIN 26 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 237 POTENTIAL.
FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 163 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 175 202 MISSING (IN SOLUBLE ISOFORM).
FT VARIANT 207 207 A -> S.
FT CONFLICT 215 215 W -> L (IN REF. 2).
SQ SEQUENCE 273 AA; 30645 MW; A7FC899B592A7967 CRC64;

Query Match 80.6%; Score 855; DB 1; Length 273;
Best Local Similarity 82.3%; Pred. No. 6,1e-60;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMITLKYVAG 60
QY 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDDVCEVENS 120
DB 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLKIVDDVLCMEENAP 120
QY 121 KDLKFSKPEPRLEFPEEFRIENRSDAFKDFVVAASESDCVSSTLSPEKDSRVAT 180
DB 121 KNIKESKRPETRSFTPEEFSTFNRSIDAFKDFVVAASDTSVLSSTLGPEDKSRVAT 180
QY 181 KPEMLPVAASSLRNDSSSNSK 203
DB 181 KPEMLPVAASSLRNDSSSNSK 203

RESULT 6
SCF_CHICK STANDARD; PRT; 287 AA.
ID SCF_CHICK
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9373244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -I- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MARELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNGESTICALLY WITH OTHER CYTOKINES,
CC PROBABLY INTERLEUKINS.
CC -I- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.
CC -I- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13516; BAA02733.1; -.
CC PIR: J0637; J0637.
CC InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.
KW Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.
FT CHAIN 1 25
FT DOMAIN 26 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 246 POTENTIAL.
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 117 BY SIMILARITY.
FT DISULFID 68 167 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 32328 MW; 6AE856AD0C152578 CRC64;

Query Match 53.0%; Score 562.5; DB 1; Length 287;
Best Local Similarity 54.6%; Pred. No. 4,3e-37;
Matches 113; Conservative 36; Mismatches 53; Indels 5; Gaps 3;

QY 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMITLKYVAG 60
QY 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLVINIVDDVCEVENS 117
DB 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLKIVDDVLCMEENAP 117
QY 118 NSSKD-LKSKFSKPEPRLEFPEEFRIENRSDAFKDFVVAASESDCVSSTLSPEKDSRVAT 175
DB 121 DNKDFIKENGLHYEDREFIPENFRLEFNSTLEYKEFADSLDNDCMPSTVEPENDS 180
QY 176 RVSATKPEMLPVAASSLRNDSSSNS 202
DB 181 RVSATKPEMLPVAASSLRNDSSSNS 207

RESULT 7
SCA4_RICE STANDARD; PRT; 981 AA.
ID SCA4_RICE
AC Q9AJ37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Antigenic heat-stable 120 kDa protein (Pst120) (120 kDa antigen)
DE (Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=42862;
RN [1]
RP SEQUENCE FROM N.A.
RX Sekeyova Z., Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
RT gene D coding for an intracytoplasmic protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -----
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CC -----
CC EMBL: AF196973; AAK31304.1; -.

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KW Antigen. 1 1
 FT NON_TER 981 981
 SQ SEQUENCE 981 AA; 107514 MW; 7F18F421E2C262E1 CRC64;

Query Match 9.68; Score 102; DB 1; Length 981;
 Best Local Similarity 23.88; Pred. No. 1.6;
 Matches 62; Conservative 34; Mismatches 87; Indels 78; Gaps 14;

OY 19 FNPVLTGEGICRNRYNNVND-----VTKLVANLPKDYMITLKYPGM-DV 63
 DB 628 FNTAKTETAI--QVNTTKVLDSPKAKELGKGTLESTIRKVAESPLNQDADYKKGGEA 685
 OY 64 LPSH-----CWISEMVQVSDSLTDLIDK-----FSNISEGLNSTVST----- 100
 DB 686 IASHKTMAPTEKISTIESEVGEVASEITDLEDKKLTGKLEGEYIEKANPEITSEKTKA 745
 OY 101 ----IDKLVNIVD-----LVECVKE-----NSSKDKK-SFKSPPEPLFTPEEPRIF 144
 DB 746 VSRGIDKSTAIPEKQALKDANEAALDRETQNLTEGKRNGLCEPKPR-----DDYNKA 801
 OY 145 NRSIDAFKDFV-----ASETSDCVYSSSTLSPEND-SRVSVTK-----PFMLPP 187
 DB 802 QDVADALKNVITPVLDAHPEKREVESEE-VYKKTSTILNDISKLAIEKVNFRAMLSPD 860
 OY 188 VAASSLRDSSSSNSKTYTL 208
 DB 861 GNLKTELEKKAESTKRVVELV 881

RESULT 8

COPG_YEAST STANDARD: PRT: 935 AA.

AC P32074;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coatomer gamma subunit (Gamma-coat protein) (Gamma-COP).
 GN SEC21 OR YNL287W OR N0543.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93096049; PubMed=1461285;
 RA Hosobuchi M.M., Kreis T., Schekman R.;
 RT "SEC21 is a gene required for ER to Golgi protein transport that
 RT encodes a subunit of a yeast coatomer.";
 RT Nature 360:603-605(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Messenguy F., Dubois F., Vierendeels F., Scherrens B., Pierard A.,
 RA Glansdorff N.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
 CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
 CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
 CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
 CC TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
 CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
 CC -1- SUPRACELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
 CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
 CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE COPG FAMILY.

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CC EMBL: M59708; AAA34598.1; -;
 DR EMBL: 271563; CA96204.1; -;
 DR PIR: A33151; A33151.
 DR PIR: S28915; S28915.
 DR SGD: S0005231; SEC21.
 DR InterPro: IPR002553; Adaptin_N.
 DR Pfam: PF01602; Adaptin_N: 1.
 KW Transport; Protein transport; Golgi stack; Membrane.
 FT CONFLICT 353 353 D -> N (IN REF. 1).
 SQ SEQUENCE 935 AA; 104830 MW; 99DC7D737DAE761 CRC64;

Query Match 8.7%; Score 92; DB 1; Length 935;
 Best Local Similarity 22.4%; Pred. No. 9.1;
 Matches 51; Conservative 40; Mismatches 79; Indels 58; Gaps 11;

OY 20 NPLVTEGICRNRYNNVNDV-TLVANLPKDYMITLKYPGM-----DVLPSHCWSE-- 72
 DB 149 HPSISAAALCTSYHLLPISEVTIRFPTNETQEAVIDLKQFPNQHGNSEIYPSNTIISQYH 208
 OY 73 ---MVQLSD---SLTDLDFKFSNISGLSNYSIIDKLVNIVDLY----- 112
 DB 209 ALGLVQLKTKDKMALKLVHRHSE-NNSMKNQALKVELVKNLIVNDLPQLFSQFRLP 267
 OY 113 -----ECYKENSCKLKSFKSPPEPLTTPPEEFTIFNRSIDAFKDFVVASETDC 163
 DB 268 LSDMLSNKRESVQLETFK-LITSFATRNSRLVAPE---LYAAISALQSLTLTPRVVSR 322
 OY 164 VVS-----STLSPKDSRVSVTKPFMLPVAASSLRDSSSSNSKY 204
 DB 323 FAALRLILNRISWVSPK---IWCNPDL-----ESLINDSRNISTY 361

RESULT 9

MYSC_HUMAN STANDARD: PRT: 1742 AA.

AC Q9NOX4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin Vc (Myosin 5C).
 GN MYO5C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodriguez O.C., Cheney R.E.;
 RT "Cloning and characterization of myosin Vc, a third member of the
 RT myosin V family in vertebrates.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 6 IQ DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.

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CC EMBL: AF272390; AAF78783.1; -;
 DR InterPro: IPR002710; DIL.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.

DR Pfam; PF01843; DIL; 1.
 DR Pfam; PF00063; myosin_head; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR Prodom; PD000355; myosin_head; 1.
 DR Prodom; PD003376; DIL; 1.
 DR SMART; SM00015; IQ; 5.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 4.
 DR Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KW Coiled coil; Polymorphism.
 FT DOMAIN 1 755 MYOSIN HEAD-LIKE.
 FT DOMAIN 756 779 IQ 1.
 FT DOMAIN 780 806 IQ 2.
 FT DOMAIN 807 829 IQ 3.
 FT DOMAIN 830 854 IQ 4.
 FT DOMAIN 855 884 IQ 5.
 FT DOMAIN 884 1351 COILED COIL (POTENTIAL).
 FT DOMAIN 1574 1679 DIUTRE.
 FT VARIANT 522 522 P -> L.
 FT VARIANT 634 634 /FTID=VAR_010646.
 FT VARIANT 634 634 L -> S.
 FT VARIANT 634 634 /FTID=VAR_010647.
 SO SEQUENCE 1742 AA; 202793 MW; 25DD3082A7EB5AAB CRC64;

Query Match 8.5%; Score 90.5; DB 1; Length 1742;
 Best Local Similarity 23.4%; Pred. No. 25;
 Matches 43; Conservative 33; Mismatches 73; Indels 35; Gaps 9;

QY 38 KDTKLVANPKRYM--TLTKVPGMDVPSHCWISENVQISDLD--LIDKFSN-- 90
 Db 1369 EDAKLIQNLIDLPKRGVYVNMIPG---LPAH--ILFMCVRADSLDANMLKSLMNST 1423
 QY 91 -----ISEGLSNYSIIDKLVINIVDIVECVKENSRLKSKSFSPERL-----FTPE 138
 Db 1424 INGIKQVKEHLEDFEMLSEWLSNTHFLNCLKQYSGEEFPMKHSPPQNNKCLNEDLS 1483
 QY 139 EFRIRNR-SIDAFKFFVAASFTS--DCVYSSITLSPKDSRVSVTKPEMLPVAASLTNR 195
 Db 1484 EYQQLISDAIRIHOIIMEKNIQPIIVPGMLEYESLQGISGLKPF-----TGFRK 1535
 QY 196 DSSS 199
 Db 1536 RSSS 1539

RESULT 10
 PTP3_DICDI
 ID PTP3_DICDI STANDARD; PRT; 989 AA.
 AC P54637;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-phosphatase phosphohydrolase 3)
 GN (PTPC1 OR PTP3) AND (PTPC2 OR PTP3).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=96189126; PubMed=8628311;
 RA Gamber M., Howard P.K., Hunter T., Firtel R.A.;
 RT Multiple roles of the novel protein tyrosine phosphatase PTP3 during Dictyostelium growth and development.
 RL Mol. Cell. Biol. 16:2431-2444(1996).
 CC -1- FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 kDa (P130).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: IN THE ANTERIOR-LIKE AND PRESTALK CELL TYPES.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH

CC AND DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U38197; AAC47041.1; -.
 DR HSSP; Q06124; 2SHP.
 DR DICTYDB; DD01111; PTPC1.
 DR DICTYDB; DD07272; PTPC2.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_prot_phptase.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase.
 FT ACT_SITE 649 649 BY SIMILARITY.
 FT DOMAIN 460 716 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 64 71 POLY-ASN.
 FT DOMAIN 109 118 POLY-ASN.
 FT DOMAIN 137 190 POLY-ASN.
 FT DOMAIN 249 257 POLY-SER.
 FT DOMAIN 258 265 POLY-SER.
 FT DOMAIN 286 289 POLY-THR.
 FT DOMAIN 286 371 POLY-ASN.
 FT DOMAIN 366 371 POLY-SER.
 FT DOMAIN 787 790 POLY-GLN.
 FT DOMAIN 834 839 POLY-GLN.
 FT DOMAIN 883 892 POLY-GLN.
 FT DOMAIN 906 914 POLY-ASN.
 FT DOMAIN 943 963 POLY-ASN.
 SO SEQUENCE 989 AA; 109995 MW; 9371105AF80974AF CRC64;

Query Match 8.4%; Score 89; DB 1; Length 989;
 Best Local Similarity 19.5%; Pred. No. 17;
 Matches 33; Conservative 37; Mismatches 61; Indels 38; Gaps 6;

QY 71 SEMVQUSDLTDLDFKSNISEGLSNYSIIDKLVN-IVDIVECVKENSRLKSKFK- 128
 Db 677 SQNMISINDVLELRQRGMVOTLDQYIFLFKVINVLIDM-GIRSLSPSKRRCEM 734
 QY 129 ---SPEPRL-----FTPEFRIRFNSIDAFKFFVAASFTSDCV----- 164
 Db 735 IKSTPMPLDISIPPLTFPPKDFOSSISPTMIASLTITQVTLKPPQOQDNDP 794
 QY 165 ---VSSITLSPKDSRVSVTK-----PFMLPVAASLRNDSSNSK 203
 Db 795 SKSKIKTSPSLNINISIRKNOQFQHPFQIQQLDNLQOQOQOQSSQ 843

RESULT 11
 UN13_CAEL
 ID UN13_CAEL STANDARD; PRT; 1815 AA.
 AC P27715;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Photol ester/diacylglycerol-binding protein unc-13.
 GN UNC-13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae.
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Maruyama I.N.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE=91288338; PubMed=2062851;
 RX Maruyama I.N., Brenner S.;
 RT "A phorbol ester/diacylglycerol-binding protein encoded by the unc-13
 gene of *Caenorhabditis elegans*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5729-5733(1991).
 RN [3]
 RP SEQUENCE OF 1-66 FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Rakow T.L., Bender J., Maruyama H., Maruyama I.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP ZINC AND PHORBOL-ESTERS BINDING.
 RX MEDLINE=93075060; PubMed=1445255;
 RA Ahmed S., Maruyama I.N., Kozma R., Lee J., Brenner S., Lim L.;
 RT "The *Caenorhabditis elegans* unc-13 gene product is a phospholipid-
 dependent high-affinity phorbol ester receptor.";
 RL Biochem. J. 287:995-999(1992).
 CC -1- FUNCTION: MAY FORM PART OF A SIGNAL TRANSDUCTION PATHWAY,
 TRANSDUCING THE SIGNAL FROM DIACYLGLYCEROL TO EFFECTOR
 CC FUNCTIONS. ONE SUCH FUNCTION COULD BE THE RELEASE OF
 CC NEUROTRANSMITTER FROM NEURONS.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THIS PROTEIN ARE PRODUCED
 CC BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE PHORBOL ESTER BINDING ACTIVITY IS ZINC AND CALCIUM-
 CC DEPENDENT.
 CC -1- MISCELLANEOUS: MUTATIONS IN UNC-13 CAUSE DIVERSE NERVOUS SYSTEM
 CC DEFECTS.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
 CC -----
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 CC -----
 DR EMBL: M62830; AAA93094.1; -;
 DR EMBL: U50735; AAA9780.1; -;
 DR EMBL: U50735; AAA9781.1; -;
 DR PIR: A41101; A41101.
 DR HSSP: P28867; IPTO.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR Pfam: PF00168; C2_3.
 DR Pfam: PF00130; DAG_PE-bind; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00008; DAGPEDOMAIN.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00239; C2; 3.
 DR PROSITE: PS00499; C2_DOMAIN_1; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 2.
 DR PROSITE: PS50047; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
 KW Phorbol-ester binding; Zinc; Repeat; Phosphorylation;
 KW Alternative splicing;
 FT DOMAIN 686 745 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 819 911 C2 DOMAIN 1.
 FT DOMAIN 1651 1740 C2 DOMAIN 2.
 FT MOD_RES 854 854 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 1341 1341 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 1689 1689 PHOSPHORYLATION (POTENTIAL).
 FT VARSPPLIC 1 85 MDNGSDYNDLDSGMSGLCTITKRRLOGAVDEFN
 STYVTKLTQVAKSTIVAVANGNLPCMEQEFIFETNRPDDG

FT VARSPPLIC 1 14 MVLMLWAKG -> MGOR (IN SHORT ISOFORM).
 FT SEQUENCE 1815 AA; 207544 MW; 8E6AABD083EBC74C CRC64;
 SQ SEQUENCE 1815 AA; 207544 MW; 8E6AABD083EBC74C CRC64;
 Query Match 8.4%; Score 89; DB 1; Length 1815;
 Best Local Similarity 18.3%; Pred. No. 35;
 Matches 40; Conservative 45; Mismatches 80; Indels 54; Gaps 8;
 QY 5 QWILTCIYLQILLRPLVKTGICRNVTNVRVTLVNLPRDVMITLKYPGMDVL 64
 DB 1490 ELWKITIVMEKRYVLPPLSDKALKQLPNAKIGVTKLMTST-----NNOSIKGM--- 1539
 QY 65 PSHCWISEMVVQLSDSLDLDFKFSNISSEGLSNYSIIKLVNIYDDIVECVKEN---SSK 121
 DB 1540 -----NSVKMMAMARE-----SEKLTFRQCIVLDCALDAIKDSFHASGK 1580
 QY 122 DLKRSFSEPRFLTPPEEFRIENRISID-AFKQEVVASTSCVVSSTLSPEKD---SRV 177
 DB 1581 GLKRSFSEPRFLTPPEEFRIENRISID-AFKQEVVASTSCVVSSTLSPEKD---SRV 177
 QY 178 SVTKPMLPP-----VAASLRNDSSSSNSKYI 205
 DB 1634 SYQVDLFSPHGTGEQKATVKTILANLDRMOTSSAKRPV 1672
 RESULT 12
 VNC5.JCDNV STANDARD; PRT; 545 AA.
 AC Q90054;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
 GN NS1
 OS *Junonia coenia* densovirus (JCDNV).
 OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
 OC NCBI_TaxID=12524;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93033112; PubMed=1413502;
 RA Dumas B., Jourdan M., Pascaud A.M., Bergoin M.;
 RT "Complete nucleotide sequence of the cloned infectious genome of
 RT *Junonia coenia* densovirus reveals an organization unique among
 RT parvoviruses.";
 RL Virology 191:202-222(1992).
 CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: S47266; AAB23699.1; -;
 DR InterPro: IPR001257; Parvo_NS1.
 DR Pfam: PF01057; Parvo_NS1; 1.
 KW Nonstructural protein.
 SQ SEQUENCE 545 AA; 63461 MW; 97CD825268ABGCAE CRC64;
 Query Match 8.3%; Score 88.5; DB 1; Length 545;
 Best Local Similarity 24.7%; Pred. No. 9;
 Matches 44; Conservative 28; Mismatches 71; Indels 35; Gaps 9;
 QY 57 YVPGMDVLPBHCWSEMV-----VOLSDSLDLDFKFS-NISEGLSNYSIIKLVNIYDDVL 111
 DB 82 YVPGQSTKPSAVISYIILRDQLRQCDVLRREGRSRNRLPFGPSEGHIIHYIH- 140
 QY 112 VECVKEN-SSMDL-----KSFSEPRFLTPPEEFRIENRISID-AFKQEVVASTSCV 164

D6 141 --CSYINRSCRIWTLSQKPPGSGV-KTGKPVAFIEFKRTMDYVIFYFYKRGERRAI 197

D5 165 V---SSTLSPEKOSRVSTKPEMLPYAAS-----SLRNDSSSNXK 203

D4 198 YVRGEGSKIPSNDECVKMTREFKREKRVSSDCTDYIEEQDQEHKISRSDAGSGNGR 255

RESULT	13	
CAPP_MEDSA		
ID		
CAPP_MEDSA		
AC	002735:	
		STANDARD;
		PRT;
		966 AA..

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Phenoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE)
GN PEPC.

0C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
0C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae
0C eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
0X NCBI_TaxID=3879;

RA Patchirana S.M., Vance C.P., Miller S.S., Gantt J.S.;
RT Alfalfa root nodule phosphoenolpyruvate carboxylase:
MEDLINE=93043034; PubMed=1421147;

RL. Plant Mol. Biol. 20:437-450(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SMRATN=CV SAPANNC.
CC

-I- CATALYTIC ACTIVITY: Phosphate + oxalacetate = H₂O + SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.

```

0Y      2 KKTQWILTCIYLOLLNPN-LVTTEGICRRRVYNNKQVTKLVANL PKD-----YMTIK 56
Db      479 EKROEMLLSELICRPLPGPDLPODET-----RDVLDFFVLAELPSDFNAGIITISMA 533
0Y      57 YVP-----GMDVLPSCHWISE--MVVOLSLSLTLDLFKNSISEGSLSVSIIDKLVIYVD 110
Db      533 TAPSVLAVELLQRECKKRNPLRVVPLFEKIDDL-----ESRPAALARLPSIDWYINRIDG 568
0Y      111 LVECV--KENSCKDLK-----SEKSPERPLFPPEEP 140
Db      589 KQEWVIGYSDSGKDAGRFSAAWOLYTKAQOEDLITKAQKF 626

```

RESULT	14	
ID	2AAA_CAEEL	
AC	009543:	STANDARD;
		PRT;
		664 AA.

DT	01-NOV-1997 (Rel. 35, last sequence update)
DT	16-OCT-2001 (Rel. 40, last annotation update)
DE	Probable protein phosphatase PP2A regulatory subunit (Protein phosphatase PP2A regulatory subunit A).
DE	phosphatase PP2A regulatory subunit A).

0S Caenorhabditis elegans.
0C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
0C Rhabdilitidae; Peloderinae; Caenorhabditis.
0X NCBI_TaxID=62339;

Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

Query Match 8.2%; Score 87; DB 1; Length 664;
 Best Local Similarity 23.2%; Pred. No. 15;
 Matches 35; Conservative 32; Mismatches 50; Indels 34; Gaps 6;

Query 12 IYQLLNFNLYVTE-----GICRNVNKKVTKLVANLPKDYMITLKYVPG 60
 Db 495 VRLAIVGFEMPLASQLGQEFDEKLLPLCLNMLTDHVFSTREASTLIMKE--LTKF--- 549
 QY 61 MDVLPSCHWISEWVYQISDLSL--TDLIDK-----FSNISGLSNYSIIDKLVINIVDDL 111
 Db 550 -----GGQMASTNIVPRMOKLQKDTNVLQRMTCLEFCINTLSEAMTQEQILKEIMPIVKDL 604
 QY 112 VE---CVKENSCKDKKSKFSKSPPEPLTPE 138
 Db 605 VEDDVVPRFNAKSLKRIKGNLPTITSE 635

RESULT 15
 BRO1_YEAST STANDARD; PRT; 844 AA.
 ID BRO1_YEAST Q02823;
 AC P48582; Q02823;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BRO1 protein.
 GN BRO1 OR YPL084W OR LPR2.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae.
 OX NCBI_TaxID:4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96220442; PubMed=8649366;
 RA Nickas M.E., Yaffe M.P.;
 RT "BRO1, a novel gene that interacts with components of the
 RT PKC β -mitogen-activated protein kinase pathway in Saccharomyces
 RT cerevisiae.";
 RL Mol. Cell. Biol. 16:2585-2593(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Hall J., Ahmed A., Bussey H., Forlin N., Friesen J.D., Storms R.K.,
 RA Vo D.H., Wang Y., Minnett E.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INTERACTS WITH COMPONENTS OF THE PKC1-MAP KINASE
 CC PATHWAY.
 CC -!- SIMILARITY: SOME, TO C.ELEGANS R10E12.1.
 CC
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 CC EMBL; U37364; AAB07790.1; -;
 DR EMBL; U41849; AAB68255.1; -;
 DR SGD; S0006005; BRO1.
 DR InterPro; IPR004328; BRO1.
 DR Pfam; PF03097; BRO1; 1.
 DR CONFLICT 359 359 Y -> C (IN REF. 2).
 FT SEQUENCE 844 AA; 97335 MW; 344905ADB845FFFB CRC64;
 SQ

Query Match 8.2%; Score 86.5; DB 1; Length 844;
 Best Local Similarity 26.3%; Pred. No. 22;
 Matches 47; Conservative 27; Mismatches 74; Indels 31; Gaps 9;

Query 30 RNRVTNNKDYTKLVANLPKDYMITLKYVGMV---LPSCHWISEWVQISDLSLIDLD 86
 Db 578 RDEINND--DITKILLINKGKSDVELKDLFEVELEKEEPSTRLEATYKQSSMIDDIKA 635
 QY 87 KFSNISGLSNYSIIDKLVINIVDDLYECYKENS--SKDLKSKFSKSPPEPLFT 136
 Db 636 KLDETFH--LSNFKDKSSGEEKFLEDKRNFPKLOEAVKSFISFSDLPKGI----- 685
 QY 137 PEEFF-RIFNRSIDAFKDFVVASETSDCVSSTLS--PEKDSRVSVT-KPPMLPPVAAS 191
 Db 686 --EFYDSLFNMSRDLAERVRAKQTEDSTANSAPAPILPILDSKASVVGEPPLLPQKSA 742

Search completed: August 18, 2002, 13:02:05
 Job time: 50 sec

Sun Aug 18 14:09:02 2002

us-09-604-325a-46.rsp

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 114.11 seconds
(without alignments)
315.336 Million cell updates/sec

Title: US-09-604-325A-46
Perfect score: 1061
Sequence: 1 MKKTQWTILTCIYLQLLFN.....AASSLRNDSSSSNKYIYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-archaea:.*
2: SP-bacteria:.*
3: SP-fungi:.*
4: SP-human:.*
5: SP-invertebrate:.*
6: SP-mammal:.*
7: SP-mhc:.*
8: SP-organelle:.*
9: SP-phage:.*
10: SP-plant:.*
11: SP-rodent:.*
12: SP-virus:.*
13: SP-vertebrate:.*
14: SP-unclassified:.*
15: SP-virus:.*
16: SP-bacteriopl:.*
17: SP-archaeop:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908.5	85.6	274	6	P79169
2	889.5	83.8	267	6	P79368
3	886.5	83.6	274	6	Q28132
4	885.5	83.5	274	6	Q95M19
5	883.5	83.3	261	6	Q95MD2
6	877	82.7	245	4	Q9UOK7
7	861	81.1	273	11	Q9QWZ4
8	859.5	81.0	274	6	Q95N18
9	855	80.6	273	11	Q64384
10	848	79.9	273	11	Q62524
11	847	79.8	273	11	P97332
12	831.5	78.4	256	6	Q62765
13	725.5	68.0	245	6	Q95MNS
14	721	68.0	245	11	Q922E7
15	716	67.5	245	11	Q64222
16					

17	570.5	53.8	287	13	Q90314	Q90314 coturnix co
18	509	48.0	123	11	Q61854	Q61854 mus musculu
19	479.5	45.2	253	13	Q90315	Q90315 coturnix co
20	401.5	37.8	96	6	Q95M8	Q95M8 equus caball
21	327	30.8	271	13	Q9YGP2	Q9YGP2 ambystoma m
22	214.5	20.2	51	6	Q9N1Y5	Q9N1Y5 equus caball
23	100	9.4	3072	12	Q92645	Q92645 clover yell
24	97.5	9.2	1490	5	Q19545	Q19545 caenorhabdi
25	97	9.1	1447	16	Q9PQJ8	Q9PQJ8 ureaplasma
26	96.5	9.1	1498	3	Q9P884	Q9P884 emericella
27	96.5	9.1	1498	3	Q96VK6	Q96VK6 emericella
28	94.5	8.9	576	11	Q62970	Q62970 ratius norv
29	94	8.9	1238	12	Q9EMP3	Q9EMP3 amaseta mco
30	94	8.9	1813	5	Q17665	Q17665 bacillus su
31	93.5	8.8	579	11	Q99RW2	Q99RW2 drosophila
32	92.5	8.7	164	16	P71021	P71021 drosophila
33	92.5	8.7	512	16	Q9CGA7	Q9CGA7 lactococcus
34	92	8.6	188	5	Q9VRK2	Q9VRK2 drosophila
35	91.5	8.6	976	2	Q54222	Q54222 staphylococ
36	91	8.6	317	5	Q9V1T2	Q9V1T2 drosophila
37	91	8.6	422	12	Q91L14	Q91L14 white spot
38	91	8.6	1107	3	Q12271	Q12271 saccharomyc
39	90.5	8.5	254	11	Q9J116	Q9J116 ratius norv
40	90.5	8.5	616	17	Q26384	Q26384 methanother
41	90	8.5	937	10	Q9M1A4	Q9M1A4 arabidopsis
42	90	8.5	1219	12	Q91LB1	Q91LB1 white spot
43	90	8.5	1501	3	Q96VL9	Q96VL9 botrytis ci
44	88.5	8.3	228	2	Q9XC73	Q9XC73 salmonella
45	88.5	8.3	941	10	Q9S1N0	Q9S1N0 arabidopsis

ALIGNMENTS

RESULT 1
ID P79169 PRELIMINARY; PRT; 274 AA.
AC P79169;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR.
GN SCF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97069946; PubMed=8912926;
RX Dunham S.P., Orlowski D.E.;
RT "The cloning and sequencing of cDNAs encoding two isoforms of feline
RT stem cell factor."
RL DNA Seq. 6:233-237(1996).
DR EMBL; D50833; BAA09445.1; -
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 274 AA; 30987 MW; C5B78DB4791237BE CRC64;

Query Match 85.6%; Score 908.5; DB 6; Length 274;
Best local similarity 88.2%; Pred. No. 2e-68;

Matches 180; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTQWTILTCIYLQLLFNLPVYKTEGICRNRYTNVVKDVKLVANLPKDYMTLTKYVG 60
Db 1 MKKTQWTIVICYLQLLFNLPVYKTEGICRNRYTDVVKVTKLVANLPKDYMTLTKYVG 60
QY 61 MDVLPSCWISSEWVVDLSLFDLDFKFSNISGLSNYSIIKLVIVYVDLVCYKENS 120
Db 61 MDVLPSCWISSEWVVDLSLFDLDFKFSNISGLSNYSIIKLVIVYVDLVCYKENS 120
QY 121 KDLKSKSPKSPKPLPTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKSDRSV 179

```

Db      121 ENVKSSSPERLFTPEEFRIPIRNSIDAFKLEWVASKTSECVSSTLSPKDSRSV 180
Oy      180 TKPFMLPPVAASLRNDSSSSNSK 203
Db      181 TKPFMLPPVAASLRNDSSSSNSK 204

RESULT 2
P79368      PRELIMINARY;      PRT;      267 AA.
ID          P79368
AC          P79368: 028591;
DT          01-MAY-1997 (TREMBlrel. 03, Created)
DT          01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT          01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE          STEM CELL FACTOR (FRAGMENT).
OS          Ovis aries (Sheep).
OC          Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Caprinae; Ovis.
OX          NCBI_TaxID=9940;
RN          [1]
RP          SEQUENCE OF 8-267 FROM N.A.
RC          TISSUE=OVARIAN FOLLICLE;
RX          MEDLINE=96413880; PubMed=8662240;
RA          Tisdall D.J., Quirke L.D., Galloway S.M.;
RT          "Ovine stem cell factor gene is located within a syntenic group on
RL          chromosome 3 conserved across mammalian species.";
RN          [2]
RP          Mamm. Genome 7:472-473(1996).
RC          SEQUENCE OF 8-267 FROM N.A.
RX          TISSUE=OVARIAN FOLLICLE;
RA          Tisdall D.J., Quirke L.D.;
RL          Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN          [3]
RP          SEQUENCE OF 1-202 FROM N.A.
RX          McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haly D.;
RL          Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR          EMBL: U89874; ABA49491.1; -.
DR          EMBL: Z50743; CA90620.1; -.
DR          InterPro: IPR003452; SCF.
DR          Pfam: PF02404; SCF; 1.
FT          NON_TER      267
SQ          SEQUENCE      267 AA; 30148 MW; 9DD959E4B9EC841 CRC64;

Query Match      83.8%; Score 889.5; DB 6; Length 267;
Best Local Similarity 85.8%; Pred. No. 7.7e-67;
Matches 175; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Oy      1 MKKTOWITTCITLQLLFNPLVTEGICRNRTNNVNDVTKLVANLPKDYMITLKYPG 60
Db      1 MKKTOWITTCITLQLLFNPLVHTOGICRNRTVDVTKLVANLPKDYMITLKYPG 60
Oy      61 MDVLPSCHWISEMENVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
Db      61 MDVLPSCHWISEMENVOLSVSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKEHSF 120
Oy      121 KDIKSKSPERLFTPEEFRIPIRNSIDAFAKDF-VVASETSDCVVSSTLSPKDSRSV 179
Db      121 KDIKSKSPERLFTPEEFRIPIRNSIDAFAKDF-VVASETSDCVVSSTLSPKDSRSV 179
Oy      121 ENVKSSSPERLFTPEEFRIPIRNSIDAFAKDFLEIVASTMSECVSSTLSPKDSRSV 180
Db      121 ENVKSSSPERLFTPEEFRIPIRNSIDAFAKDFLEIVASTMSECVSSTLSPKDSRSV 180
Oy      180 TKPFMLPPVAASLRNDSSSSNSK 203
Db      181 TKPFMLPPVAASLRNDSSSSNSK 204

RESULT 3
P79368      PRELIMINARY;      PRT;      274 AA.
ID          028132
AC          028132;
DT          01-NOV-1996 (TREMBlrel. 01, Created)
DT          01-NOV-1996 (TREMBlrel. 01, Last sequence update)

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DT          01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE          STEM CELL FACTOR LONGER ISOFORM.
GN          SCF.
OS          Bos taurus (Bovine).
OC          Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Caprinae; Bos.
OX          NCBI_TaxID=9913;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=SPLEEN;
RX          MEDLINE=94339176; PubMed=7520283;
RA          Zhou J., Hakono H., Ohtaki M., Kubota T., Sakurai M.;
RT          "Cloning and characterization of cDNAs encoding two normal isoforms of
RL          bovine stem cell factor.";
RN          [2]
RP          Biochim. Biophys. Acta 1223:148-150(1994).
RC          SEQUENCE FROM N.A.
RX          TISSUE=SPLEEN;
RA          Kudo T.;
RT          "Bovine counterpart of stem cell factor.";
RL          Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR          EMBL: D28934; BAA0661.1; -.
DR          EMBL: AB033716; BAA94808.1; -.
DR          InterPro: IPR003452; SCF.
DR          Pfam: PF02404; SCF; 1.
SQ          SEQUENCE      274 AA; 31014 MW; D6C1DD877B0CB12B CRC64;

Query Match      83.6%; Score 886.5; DB 6; Length 274;
Best Local Similarity 85.3%; Pred. No. 1.4e-66;
Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Oy      1 MKKTOWITTCITLQLLFNPLVTEGICRNRTNNVNDVTKLVANLPKDYMITLKYPG 60
Db      1 MKKTOWITTCITLQLLFNPLVHTOGICRNRTVDVTKLVANLPKDYMITLKYPG 60
Oy      61 MDVLPSCHWISEMENVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
Db      61 MDVLPSCHWISEMENVOLSVSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKEHSF 120
Oy      121 KDIKSKSPERLFTPEEFRIPIRNSIDAFAKDF-VVASETSDCVVSSTLSPKDSRSV 179
Db      121 KDIKSKSPERLFTPEEFRIPIRNSIDAFAKDF-VVASETSDCVVSSTLSPKDSRSV 179
Oy      121 ENVKSSSPERLFTPEEFRIPIRNSIDAFAKDFLEIVASTMSECVSSTLSPKDSRSV 180
Db      121 ENVKSSSPERLFTPEEFRIPIRNSIDAFAKDFLEIVASTMSECVSSTLSPKDSRSV 180
Oy      180 TKPFMLPPVAASLRNDSSSSNSK 203
Db      181 TKPFMLPPVAASLRNDSSSSNSK 204

RESULT 4
P79368      PRELIMINARY;      PRT;      274 AA.
ID          095M19
AC          095M19;
DT          01-DEC-2001 (TREMBlrel. 19, Created)
DT          01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT          01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE          STEM CELL FACTOR.
OS          Capra hircus (Goat).
OC          Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Caprinae; Capra.
OX          NCBI_TaxID=9925;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=SHIBA; TISSUE=BRAIN;
RA          Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT          "Identification of Splicing Isoforms of Caprine Stem Cell Factor
RL          (gSCF825 and gSCF741, in the Brain and the Skin of Adult and Fetal
RT          Suba Goats, Capra hircus).";
RL          Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR          EMBL: AB002152; BAB71753.1; -.

```

SQ SEQUENCE 274 AA; 31052 MW; BBE669A509EF65D CRC64;

Query Match 83.5%; Score 885.5; DB 6; Length 274;
Best Local Similarity 85.3%; Pred. No. 1.7e-66;
Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 120
QY 121 KDLKSFSPERLFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSY 179
DB 121 ENVKSSKSPERQRTPEKFGIFKSIDAFKDFEIYASTSECVIISSTSPKDSRVSY 180
QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 5

Q95MD2 PRELIMINARY; PRT; 261 AA.

AC Q95MD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MAAT CELL GROWTH FACTOR (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF401625; AAK94474.1; -.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 29526 MW; 16A3062105346E4B CRC64;

Query Match 83.3%; Score 883.5; DB 6; Length 261;
Best Local Similarity 86.6%; Pred. No. 2.4e-66;
Matches 174; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

QY 4 TOTWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 63
DB 1 TOTWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
QY 64 LPSHCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 123
DB 64 LPSHCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 120
QY 124 KKSFSPEPRFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSYTKP 182
DB 124 KKSFSPEPRFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSYTKP 180
QY 183 FMLPVAASSLRNDSSSSNSK 203
DB 181 FMLPVAASSLRNDSSSSNSK 201

RESULT 6
Q90UK7 PRELIMINARY; PRT; 245 AA.

AC Q90UK7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160429; PubMed=10049787;
RA Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;
RT "Parathyroid hormone-regulated production of stem cell factor in human
osteoblasts and osteoblast-like cells.";
RL Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF119835; AAD22048.1; -.
DR EMBL, AF400437; AAK92486.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 245 AA; 27903 MW; FF87983163A33C36 CRC64;

Query Match 82.7%; Score 877; DB 4; Length 245;
Best Local Similarity 98.3%; Pred. No. 7.7e-66;
Matches 170; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECVKENS 120
QY 121 KDLKSFSPERLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEK 173
DB 121 KDLKSFSPERLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEK 173

RESULT 7

Q90WZ4 PRELIMINARY; PRT; 273 AA.

AC Q90WZ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR KL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Teramoto T., Nagashima M., Thorgeirsson S.S.;
RT "Rat-SCF-KL-1.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF071204; AAD02827.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 273 AA; 30712 MW; C0F56527DC93FD27 CRC64;

Query Match 81.1%; Score 861; DB 11; Length 273;
Best Local Similarity 82.3%; Pred. No. 1.9e-64;
Matches 167; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 60

DB 121 KNKESKRPETRSFTPEEFISFNSSIDAFKDFVASDTSOVLSTLGPEDKSRVSVT 180
 QY 181 KPFLPVAASLRNDSSSSNSK 203
 DB 181 KPFLPVAASLRNDSSSSNSK 203

RESULT 11
 ID 062524 PRELIMINARY; PRT: 273 AA.

AC 062524;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/El; TISSUE=BRAIN;
 RX MEDLINE=97032534; PubMed=8875893;
 RA Graw J., Loester J., Neuhauser-Klaus A., Pretsch W., Schmitt-John T.;
 RT "Molecular analysis of two new steel mutations in mice shows a
 RT transversion or an insertion."
 RL Mamm. Genome 7:843-846(1996).
 DR EMBL: X9322; CAA67698.1; -.
 DR MGD: MGI:96974; K1L.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30645 MW; B3E9D0B72C734107 CRC64;

Query Match 79.9%; Score 848; DB 11; Length 273;
 Best Local Similarity 81.8%; Pred. No. 2.4e-63;
 Matches 166; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWITTCIYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQSLDITLDLDFKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
 DB 61 MDVLPSCWISSEMYVQSLDITLDLDFKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
 QY 121 KDLKSPKSPRLFTPEEFIRFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSPKSPRLFTPEEFIRFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASLRNDSSSSNSK 203
 DB 181 KPFLPVAASLRNDSSSSNSK 203

RESULT 12
 ID 062524 PRELIMINARY; PRT: 273 AA.

AC 062524;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF S1-3NEU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=102/ElX3H/El; Fl;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhauser-Klaus, Pretsch;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
 RT gene defines a novel allele at the steel locus with a weak
 RT phenotype."
 RL Mutat. Res., Mutat. Res. Genomics 382:75-78(1997).
 DR EMBL: Y10287; CAA71329.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

Query Match 79.8%; Score 847; DB 11; Length 273;
 Best Local Similarity 81.8%; Pred. No. 2.9e-63;
 Matches 166; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWITTCIYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQSLDITLDLDFKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
 DB 61 MDVLPSCWISSEMYVQSLDITLDLDFKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
 QY 121 KDLKSPKSPRLFTPEEFIRFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSPKSPRLFTPEEFIRFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASLRNDSSSSNSK 203
 DB 181 KPFLPVAASLRNDSSSSNSK 203

RESULT 13
 ID 062765 PRELIMINARY; PRT: 256 AA.
 AC 062765;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
 GN SCF.
 OS Equus caballus (horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
 RT "An Equine sequence homologous to stem cell factor (KIT-ligand)."
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF053498; AAC97076.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1
 FT NON_TER 1 1
 FT NON_TER 256 256
 SQ SEQUENCE 256 AA; 28933 MW; 9E4876CAEC7B55FF CRC64;

Query Match 78.4%; Score 831.5; DB 6; Length 256;
 Best Local Similarity 86.0%; Pred. No. 5.3e-62;
 Matches 166; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

QY 12 IYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVPGMDVLPSCWIS 71
 DB 1 IYQLDLFFNPLVTEGICRNRYNNKDYTKLVANLPKDYMITLKYVPGMDVLPSCWIS 71

QY 72 EMVVOUSDSTLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSSKDLKKSEKSP 131
 DB 61 EMVOHLSVSLTDLLEKFSNISSEGLSNYSIIDKLIVKLVDDLECKEENSSKDLKKSEKSP 120
 QY 132 PRLTPEEPFRIRNRSIDAFKDF-VVASSETSDCVSSTISPEKDSRVSTKPPMLPVAA 190
 DB 121 SRLTPEEPFRIRNRSIDAFKDFEMVVSSTISPEKDSRVSTKPPMLPVAA 180
 QY 191 SSLRNDSSSSNSK 203
 DB 181 SSLRNDSSSSNSK 193

RESULT 14

ID Q95MN5 PRELIMINARY; PRT; 260 AA.
 AC Q95MN5;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE STEM CELL FACTOR SHORT ISOFORM.
 OS Muscula vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OX NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett R.D., Murphy B.D.;
 RT "Stem cell factor in the mink uterus";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF323757; AAK73366.1; -.
 SQ SEQUENCE 260 AA; 29542 MW; A63111CE48A50A34 CRC64;

Query Match

Best Local Similarity 68.4%; Score 725.5; DB 6; Length 260;
 Matches 144; Conservative 21; Mismatches 21; Indels 9; Gaps 2;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCIYQLLLFNPLVKTGICRNRVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMVVOUSDSTLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVOUSDSTLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSFSPPEPRLTPEEPFRIRNRSIDAFKDF-VVASSETSDCVSSTISPEKDSRV 179
 DB 121 ENVKSPKPEPRLTPEEPFRIRNRSIDAFKDF-VVASSETSDCVSSTISPEKDSRV 179
 QY 180 TKPEMLPVAAASLR 194
 DB 180 -----PLGDSNLQ 187

RESULT 15

ID Q92ZET PRELIMINARY; PRT; 245 AA.
 AC Q92ZET;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE STEM CELL FACTOR KL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Teramoto T., Nagashima M., Thorgerirsson S.S.;
 RT "Rat-SCF-KL-2";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF071205; AAD02828.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 SQ SEQUENCE 245 AA; 27691 MW; 961511DAA6AE4F82 CRC64;

Query Match

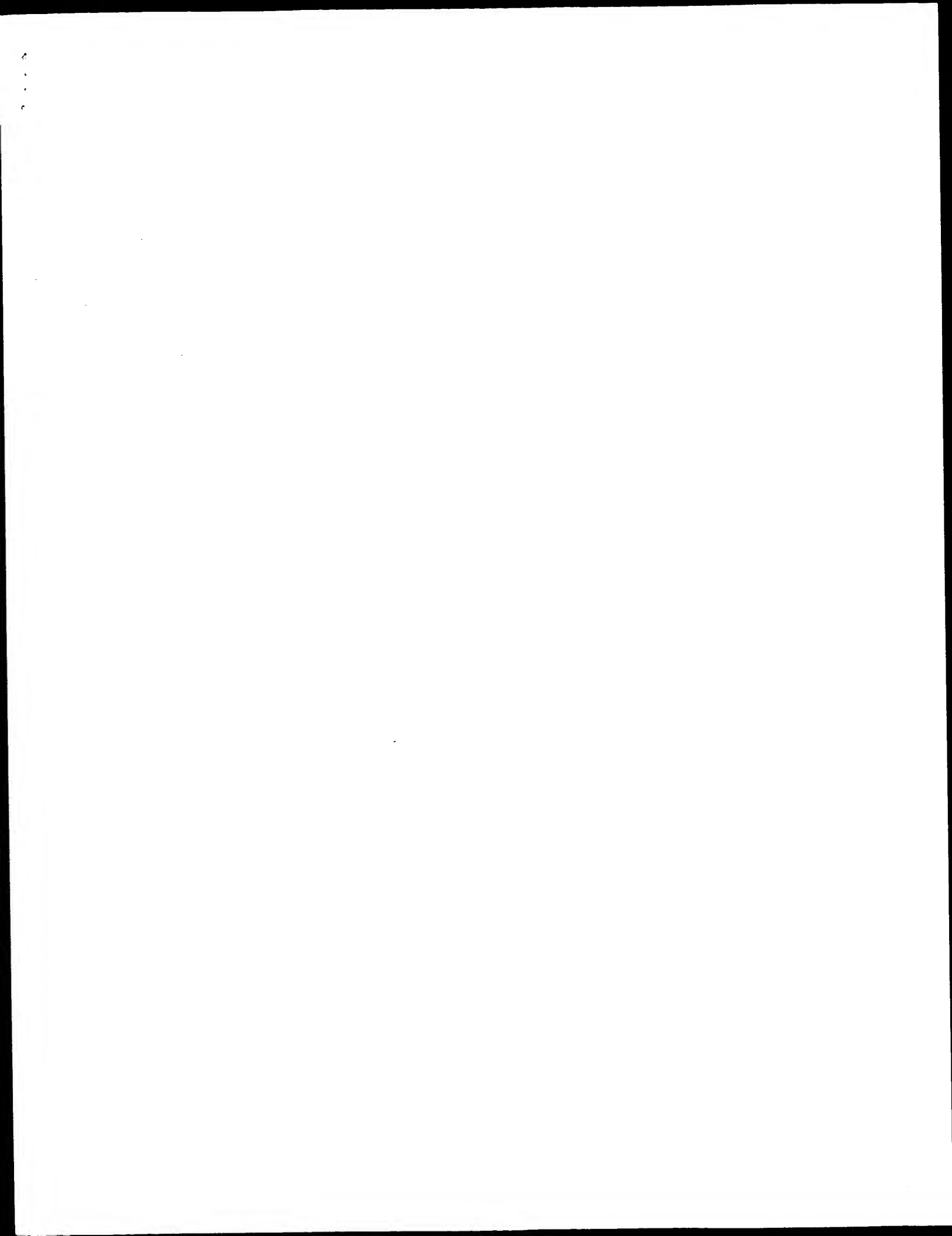
Best Local Similarity 68.0%; Score 721; DB 11; Length 245;
 Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCIYQLLLFNPLVKTGICRNRVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMVVOUSDSTLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVOUSDSTLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSFSPPEPRLTPEEPFRIRNRSIDAFKDFVVASSETSDCVSSTISPEK 173
 DB 121 KNVKSILKPEPRLTPEEPFRIRNRSIDAFKDFVVASSETSDCVSSTISPEK 173

Search completed: August 18, 2002, 13:06:04
 Job time: 289 sec

Sun Aug 18 14:09:03 2002

us-09-604-325a-46.rsp



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:08:01 ; Search time 111.53 Seconds

(without alignments)
271.883 Million cell updates/sec

Title: US-09-604-325a-61
Perfect score: 1397
Sequence: 1 MKKTQWILFCIYLQLLFN.....NEEDNEISMLQEKRESEQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_032802:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	273	12	AA11711
2	1397	100.0	273	13	AA11711
3	1397	100.0	273	13	AA11711
4	1397	100.0	273	13	AA11711
5	1397	100.0	273	13	AA11711
6	1397	100.0	273	13	AA11711
7	1397	100.0	273	13	AA11711
8	1397	100.0	273	13	AA11711
9	1397	100.0	273	13	AA11711
10	1397	100.0	273	13	AA11711
11	1397	100.0	273	13	AA11711

ALIGNMENTS

12	1397	100.0	273	22	AA11711	Human stem cell fa
13	1397	100.0	273	22	AA11711	Human stem cell fa
14	1397	100.0	273	22	AA11711	Human stem cell fa
15	1397	99.6	273	22	AA11711	Human stem cell fa
16	1397	99.6	273	22	AA11711	Human stem cell fa
17	1397	99.6	273	22	AA11711	Human stem cell fa
18	1397	99.6	273	22	AA11711	Human stem cell fa
19	1397	99.6	273	22	AA11711	Human stem cell fa
20	1397	99.6	273	22	AA11711	Human stem cell fa
21	1381	98.9	273	22	AA11711	Human stem cell fa
22	1381	98.9	273	22	AA11711	Human stem cell fa
23	1381	98.9	273	22	AA11711	Human stem cell fa
24	1381	98.9	273	22	AA11711	Human stem cell fa
25	1381	98.9	273	22	AA11711	Human stem cell fa
26	1378	98.6	273	22	AA11711	Human stem cell fa
27	1378	98.6	273	22	AA11711	Human stem cell fa
28	1378	98.6	273	22	AA11711	Human stem cell fa
29	1378	98.6	273	22	AA11711	Human stem cell fa
30	1378	98.6	273	22	AA11711	Human stem cell fa
31	1378	98.6	273	22	AA11711	Human stem cell fa
32	1378	98.6	273	22	AA11711	Human stem cell fa
33	1378	98.6	273	22	AA11711	Human stem cell fa
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35	1378	98.6	273	22	AA11711	Human stem cell fa
36	1378	98.6	273	22	AA11711	Human stem cell fa
37	1378	98.6	273	22	AA11711	Human stem cell fa
38	1378	98.6	273	22	AA11711	Human stem cell fa
39	1378	98.6	273	22	AA11711	Human stem cell fa
40	1378	98.6	273	22	AA11711	Human stem cell fa
41	1378	98.6	273	22	AA11711	Human stem cell fa
42	1378	98.6	273	22	AA11711	Human stem cell fa
43	1378	98.6	273	22	AA11711	Human stem cell fa
44	1378	98.6	273	22	AA11711	Human stem cell fa
45	1378	98.6	273	22	AA11711	Human stem cell fa

RESULT 1	AA11711	standard; Protein; 273 AA.
ID	AA11711	
AC	AA11711	
XX		
DT	20-JUN-1991	(first entry)
DE	Human Stem Cell Factor from HT1080 fibrosarcoma line.	
XX		
KW	Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..25
FT	Protein	/label= sig-peptide
FT		26..273
FT		/label= mat-protein
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PN	EP423980-A.	
XX		
PD	24-APR-1991.	
XX		
PE	04-OCT-1990.	90EP-0310899.
XX		
PR	01-OCT-1990.	90US-0589701.
PR	16-OCT-1989.	89US-0422383.
PR	11-JUN-1990.	90US-0537198.
PR	24-AUG-1990.	90US-0573616.
PR	28-SEP-1990.	90WC-US05548.
XX		
PA	(AMGE-) AMGEN INC.	
XX		

PI Zeebo KM, Suggs SV, BosseIman RA, Martin FH;
 XX
 DR WPI: 1991-119233/17.
 DR N-PSDB: AAQ11542.
 XX
 XX New naturally-occurring polypeptide stem cell factor analogues -
 PT have haematopoietic biological activity of stem cell factor and
 PT are used to treat eg leukopenia, AIDS, nerve damage and
 PT infertility
 PS Disclosure, Fig 42; 127pp: English.
 XX
 XX The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ11509-011543.
 CC
 XX
 SO Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 12; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCITCYQLLFPNPLVTEGICRRNRYNNKDYTKLVANLPKDYMITLKYPG 60
 DB 1 mktqtwilctciyqlllfnpivktegicrrnrvnkvtklvaniipkdymitlkypg 60
 QY 61 MDVLPSCHEWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 mdvlpshcwissemvqvsdsltldlfdksniseglsnysiidklvniyvdllveckvknss 120
 QY 121 KDLSKFSKSPRLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdlskfskspeprlftpeeffrifnrsidafkdfvvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSNRKAKNPBGSSLHWAMALPALFSLITGFAGALYWKRR 240
 DB 181 kpfmlpvaasslrndsssnrkaknpbgdsslnwamaalpalsliffagalywkrr 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
 DB 241 qpsltraveniqineedneismleqekerefgev 273
 RESULT 2
 AAR20647
 ID AAR20647 standard; Protein; 273 AA.
 XX
 AC AAR20647;
 XX
 DT 30-APR-1992 (first entry)
 XX
 DE Human mast cell growth factor.
 XX
 KW hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
 KM proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= signal
 FT Region 26..210
 FT /label= extracellular
 FT /note= "claimed polypeptide"
 FT Region 211..237
 FT /label= transmembrane
 FT Region 238..273

FT
 XX
 PN W09200376-A.
 XX
 PD 09-JAN-1992.
 XX
 XX 14-JUN-1991; 91WO-US04274.
 PF
 XX 25-JUN-1990; 90US-0543264.
 PR 10-AUG-1990; 90US-0565840.
 PR 28-AUG-1990; 90US-0574152.
 PR 21-SEP-1990; 90US-0586073.
 PR 12-JUN-1991; 91US-0713715.
 XX
 PA (IMMUNEX CORP.
 PI Williams DE, Lyman S;
 XX
 XX WPI: 1992-041558/05.
 DR N-PSDB: AAQ20845.
 XX
 XX New isolated DNA encoding human mast cell growth factor - useful in
 PT stimulating proliferation of haematopoietic cells with growth factor,
 PT to treat haemolytic and hypoproliferative anaemias
 PS Claim 10; Fig 4; 59pp: English.
 XX
 XX This human MGF has a mature extracellular region of 185 amino acids.
 CC There is a second form of hMGF (see AAQ20844) resulting from an
 CC alternative mRNA splicing event which deletes an exon encoding an
 CC additional 28 amino acids beginning at amino acid 148 of the mature
 CC protein. MGF is the ligand for the protein receptor expression product
 CC of the c-kit proto-oncogene. MGF can be used to augment the
 CC activity of other cytokines. It can influence early lymphoid or
 CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
 CC
 XX
 SO Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 13; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCITCYQLLFPNPLVTEGICRRNRYNNKDYTKLVANLPKDYMITLKYPG 60
 DB 1 mktqtwilctciyqlllfnpivktegicrrnrvnkvtklvaniipkdymitlkypg 60
 QY 61 MDVLPSCHEWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 mdvlpshcwissemvqvsdsltldlfdksniseglsnysiidklvniyvdllveckvknss 120
 QY 121 KDLSKFSKSPRLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdlskfskspeprlftpeeffrifnrsidafkdfvvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSNRKAKNPBGSSLHWAMALPALFSLITGFAGALYWKRR 240
 DB 181 kpfmlpvaasslrndsssnrkaknpbgdsslnwamaalpalsliffagalywkrr 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
 DB 241 qpsltraveniqineedneismleqekerefgev 273
 RESULT 3
 AAR83978
 ID AAR83978 standard; Protein; 273 AA.
 XX
 AC AAR83978;
 XX
 DT 15-MAY-1996 (first entry)
 XX
 DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.

```

XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KM thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= sig-peptide
XX Protein 26..248
XX /label= mat-SCF
XX EP676470-A1.
XX 11-OCT-1995.
XX 04-OCT-1990; 90EP-0105391.
XX 01-OCT-1990; 90US-0589701.
XX 16-OCT-1989; 89US-0423383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 28-SEP-1990; 90WO-0505548.
XX (AMGE-) AMGEN INC.
XX Bosselman RA, Martin FH, Suggs SV, Zeebo KM;
XX WPI: 1995-346090/45.
XX N-PSDB; AAT04890.
XX New stem cell factor polypeptide(s) - for stimulating the growth of
XX primitive progenitor cells, esp. for treating disorders involving
XX blood cells
XX Claim 9; Fig 42; 127pp; English.
XX AAR83978 is a human stem cell factor (SCF) derived from the HT1080
XX fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
XX truncated polypeptides, having amino acid sequences sufficiently
XX duplicative of naturally occurring SCF, stimulate growth of primitive
XX progenitors such as haematopoietic progenitor cells, neural stem
XX cells and primordial germ stem cells. The peptides can be used in a
XX composition for treating leucopenia, anaemia or thrombocytopenia,
XX for enhancing engraftment of bone marrow during transplantation or
XX for bone marrow recovery after chemotherapy or radiation-induced bone
XX marrow aplasia or myelosuppression. They can also be used for
XX treating neoplasia, nerve damage, infertility, intestinal damage or
XX myeloproliferative disorders. Antibodies may be raised against the
XX peptides for use in detection or neutralisation of SCF in serum. SCF
XX may be useful for the treatment of AIDS and severe combined
XX immunodeficiency (SCID) states alone or in combination with other
XX factors such as IL-7.
XX Sequence 273 AA:
XX
XX Query Match 100.0%; Score 1397; DB 16; Length 273;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-133;
XX Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKRTQWILTCIYQLLEFNPLVTEGICRNVRVNNVKDVTFLVNLPRDYMITLKYPG 60
XX |
XX 1 mktqtwtlctiyqlllfnplvtegeicrnrvtnnvkdvtklvnlprdymitlkyppg 60
XX
XX 61 MDVPSHCWISDMVYQVSDSLTDLDKFSNISSEGLSNTSIIDKLNIYVDLVECKENSS 120
XX |
XX 61 mdvpschcwismvvyqvsdsltldkfsnisseglsntsiidklniyvdleveckenss 120
XX
XX 121 KDLKSKFSKPEPRILFTPEEFRIINRSIDAFKDFVAVASETSCVYVSSPTLSPKDSRVSVT 180
XX |
XX 121 kdlkskfskpeprilftpeefriinrsidafkdfvavasetscvyvssptlspkdsrvsvt 180
XX
XX 121 KALKSKFSKPEPRILFTPEEFRIINRSIDAFKDFVAVASETSCVYVSSPTLSPKDSRVSVT 180
XX |
XX 121 kalkskfskpeprilftpeefriinrsidafkdfvavasetscvyvssptlspkdsrvsvt 180

```

```

XX 181 KPEMLPFAAASLINDSSSNRKAKNPBGSSSLHMAAMALPAIFSLITGFAGALYKKR 240
XX |
XX 181 kpemlpfaaaslinndsssnrkaknpbgssslhmaamalpaifslitgfaalgykkrr 240
XX
XX 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
XX |
XX 241 qpsltraventiqineedneismlqekerefev 273
XX
XX RESULT 4
XX AAM27607 standard; Protein; 273 AA.
XX ID AAM27607
XX AC AAM27607;
XX DT 28-APR-1998 (first entry)
XX DE Human recombinant stem cell factor protein.
XX KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
XX SF; SDF; analogue; treatment; haematopoietic factor; progenitor cell;
XX KW pigmentation disorder; haematopoietic disorder.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..25
XX FT /label= leader sequence
XX FT Protein 26..274
XX FT /note= "mature full length stem cell factor protein"
XX
XX FN W09738101-A1.
XX 16-OCT-1997.
XX 03-APR-1997; 97WO-US05541.
XX 05-APR-1996; 96US-0628428.
XX (AMGE-) AMGEN INC.
XX Lu HS;
XX WPI: 1997-512718/47.
XX Stem cell factor analogue NI0D or NI0D/NI1D - useful to treat
XX pigmentation disorder, AIDS, nerve damage, infertility, intestinal
XX damage or haematopoietic disorder
XX Claim 2; Fig 1; 42pp; English.
XX
XX This sequence represents a membrane bound form of a human recombinant
XX stem cell factor (SCF). Stem cell factors are also known as mast cell
XX growth factors (MCGF) or Steel factors (SF or SDF) are haematopoietic
XX factors which act on haematopoietic progenitor cells. Analogues of a
XX wild type SCF sequence have been constructed (see AAM27605 and AAM27606)
XX which have increased biological activity and stability compared to
XX unmodified SCF and can be used to treat pigmentation disorders, e.g.
XX vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility,
XX intestinal damage or a haematopoietic disorder, e.g. leucopenia,
XX thrombocytopenia or anaemia, enhance bone marrow engraftment during
XX transplantation or bone marrow recovery following radiation, chemical or
XX chemotherapeutic, induced bone marrow aplasia or myelosuppression,
XX sensitise cells to chemotherapy or mobilise peripheral blood progenitor
XX cells. It can also be used in an in vitro haematopoietic cell, preferably
XX bone marrow or peripheral blood progenitor cell, culture medium, where
XX the cells are optionally subsequently transfected with exogenous DNA.
XX Sequence 273 AA:
XX
XX Query Match 100.0%; Score 1397; DB 18; Length 273;

```

Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVKKVYANLPKDYMTLKYVPG 60
Db 1 mktqwtlctiyqlllfnplvktgicrnrytnvkvkvanlpkdymltkyvp 60

QY 61 MDVLPSCWISSEWVQVSDSLDLDKFSNISEGLSNYSIIIRKLVNIYVDLVCVENSS 120
Db 61 mdvlpshcwissemvqvsdldldkfnsiseglsnyslidlkvniyvdldvcvknss 120

QY 121 KDILKSFSPERPLFTPEEFRIFNRSIDAFKDVVASTSDCVSSTLSPKDSRVSVT 180
Db 121 kdilksfkspeprlftpeeffrifnrsidafkdvvasetsdcvsvstlspkdsrvsvt 180

QY 181 KPMLPPVAASSLRNDSSSNRKAKNPBGSSLHWAMALPALFSLITGAFGALYWKRR 240
Db 181 kpmlppvaasslrndsssnrkaknpbgdsslhwaamalpalfslltgafgalywkkrr 240

QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
Db 241 qpsltraveniqineedneismqekerefgev 273

RESULT 5
ID AAY53284 standard; Protein; 273 AA.
XX AAY53284;
AC AAY53284;
DT 27-JUL-2000 (first entry)
XX
XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX primitive progenitor cell; haematopoietic disorder; synergistic;
XX allogenic; autologous bone marrow transplant; gene therapy;
XX transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX cancer.
XX
XX Homo sapiens.
XX
XX EP992579-A1.
XX
XX 12-APR-2000.
XX
XX 04-OCT-1990; 99EP-0122861.
XX
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 28-SEP-1990; 90WO-US05548.
XX 01-OCT-1990; 90US-0589701.
XX 04-OCT-1990; 90EP-0310899.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Suggs SV, Bosseimann RA, Martin FH;
XX
XX MPI: 2000-259135/23.
XX N-PSDB; AAA13714.
XX
XX Production of hematopoietic cells suitable for administration to a
XX subject using progenitor cells and expanding the cells using stem cell
XX factor -
XX
XX Claim 22; Fig 42; 123pp; English.
XX
XX A method has been developed of making haematopoietic cells suitable for
XX administration to a subject. The method comprises: (a) obtaining
XX haematopoietic progenitor cells from a donor; and (b) expanding the
XX cells by adding to the cells a haematopoietically effective dose of a
XX polypeptide product having at least part of the primary structural

CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early hematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is
CC useful for expanding early haematopoietic progenitors in synergistic,
CC allogenic or autologous bone marrow transplant. SCF is useful for
CC enhancing the efficiency of gene therapy based on transfecting the
CC haematopoietic stem cells. SCF is also useful for combating the
CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
CC haematopoietic recovery after acute blood loss and as a boost to the
CC immune system for fighting neoplasia (cancer). The present sequence
CC represents a specifically claimed human SCF from the present invention.
XX
XX Sequence 273 AA:
SO

Query Match 100.0%; Score 1397; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVKKVYANLPKDYMTLKYVPG 60
Db 1 mktqwtlctiyqlllfnplvktgicrnrytnvkvkvanlpkdymltkyvp 60

QY 61 MDVLPSCWISSEWVQVSDSLDLDKFSNISEGLSNYSIIIRKLVNIYVDLVCVENSS 120
Db 61 mdvlpshcwissemvqvsdldldkfnsiseglsnyslidlkvniyvdldvcvknss 120

QY 121 KDILKSFSPERPLFTPEEFRIFNRSIDAFKDVVASTSDCVSSTLSPKDSRVSVT 180
Db 121 kdilksfkspeprlftpeeffrifnrsidafkdvvasetsdcvsvstlspkdsrvsvt 180

QY 181 KPMLPPVAASSLRNDSSSNRKAKNPBGSSLHWAMALPALFSLITGAFGALYWKRR 240
Db 181 kpmlppvaasslrndsssnrkaknpbgdsslhwaamalpalfslltgafgalywkkrr 240

QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
Db 241 qpsltraveniqineedneismqekerefgev 273

RESULT 6
ID AAU05266 standard; Protein; 273 AA.
XX AAU05266;
AC AAU05266;
DT 24-OCT-2001 (first entry)
XX
XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
XX Human; stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
XX blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Protein 1..25
XX Protein /label= signal_peptide
XX Protein 26..273
XX Protein /label= Mature_SCF
XX MISC-difference 97
XX FT /note= "Encoded by ATT"
XX FT MISC-difference 258
XX FT /note= "Encoded by ATT"
XX PN US6248319-B1.
XX PD 19-JUN-2001.

XX 24-MAY-1995; 95US-0449653.
 XX 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0123229.
 XX (ZSEB/) ZSEBO K M.
 PA (BOS/) BOSSSELMAN R A.
 PA (SUG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI: 2001-407312/43.
 DR N-PSDB: AAS10461.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 XX Example 3; Fig 42; 210pp; English.
 XX
 CC The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the HT1080 fibrosarcoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of human
 CC disorders, including myelofibrosis, myelodysplasia, osteoporosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 CC
 XX
 XX Sequence 273 AA;
 SQ
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQMTITCTIYIOLLEFNPLVKTGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
 DB 1 mktktqmtitctiyiqllfnplvktgicrnrvnnvadvklvanlpkdymltklyvpg 60
 QY 61 MDVLPSCWISSEMYVQSDSLTDLLDKFSNISEGLSNYSIIDKLVNIYVDLVECVKENSS 120
 DB 61 mdvlpshcwisemvqvdsdltldlksniseglsnysiidklvniyvdllvecvkenss 120
 QY 121 KDLKSFKSPERPLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdlksfksperrltppeeffrifnrsidafkdfvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFMLPPVAASSLRNDSSSNKRAKNPBGDSSLHMAAALPALFSLITIGFAGALYWKRR 240
 DB 181 kpfmlppvaasslrndsssnkraknpbgdsslhmaaalpalfslitigfagalylwkr 240
 QY 241 QPSLTRAVENIQINEEDNEISMLOKEREFOEV 273
 DB 241 qpsltraveniqineedneismloqekerefev 273
 RESULT 7
 AAB98357

ID AAB98357 standard; Protein; 273 AA.
 XX
 XX AAB98357;
 AC
 XX 21-AUG-2001 (first entry)
 DT
 XX Human SCF protein SEQ ID NO:49.
 DE
 XX Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 XX gene therapy.
 XX Homo sapiens.
 OS
 XX US6207454-B1.
 PN
 XX 27-MAR-2001.
 PD
 XX 31-DEC-1998; 98US-0224681.
 PF
 XX 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR (AMGE-) AMGEN INC.
 PA
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI: 2001-36062/38.
 DR
 XX Enhancing efficiency of transfer of polynucleotide into a target
 XX mammalian cell in vitro, involves exposing cell that expresses a stem
 XX cell factor receptor to stem cell factor, and introducing
 XX polynucleotide into cell in vitro -
 XX
 XX Example 3; Fig 16; 210pp; English.
 XX
 CC The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 CC
 XX
 XX Sequence 273 AA;
 SQ
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQMTITCTIYIOLLEFNPLVKTGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
 DB 1 mktktqmtitctiyiqllfnplvktgicrnrvnnvadvklvanlpkdymltklyvpg 60
 QY 61 MDVLPSCWISSEMYVQSDSLTDLLDKFSNISEGLSNYSIIDKLVNIYVDLVECVKENSS 120
 DB 61 mdvlpshcwisemvqvdsdltldlksniseglsnysiidklvniyvdllvecvkenss 120
 QY 121 KDLKSFKSPERPLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdlksfksperrltppeeffrifnrsidafkdfvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFMLPPVAASSLRNDSSSNKRAKNPBGDSSLHMAAALPALFSLITIGFAGALYWKRR 240
 DB 181 kpfmlppvaasslrndsssnkraknpbgdsslhmaaalpalfslitigfagalylwkr 240

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Db      181 kpfmlppvaasslrndsssnrkaknpqgsslhwaamalpalflsligfagalywkkrr 240
QY      241 QPSLTRAVENIQINEEDNEISMLOEKEREPOEV 273
Db      241 qpsltraveniqineedneismloekerefev 273

RESULT 8
AAB98367
ID      AAB98367 standard; Protein; 273 AA.
XX
AC      AAB98367;
XX
DE      21-AUG-2001 (first entry)
XX
DE      Human SCF protein sequence SPO ID NO:61.
XX
KW      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW      gene therapy.
XX
OS      Homo sapiens.
XX
PN      US6207454-B1.
XX
PD      27-MAR-2001.
XX
PE      31-DEC-1998; 98US-0224681.
XX
PR      21-DEC-1993; 93US-0172329.
PR      24-MAY-1995; 95US-0449653.
PR      12-JAN-1998; 98US-0005893.
PR      25-NOV-1992; 92US-0982255.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR      N-PSDB; AAH41344.
XX
XX
PT      Enhancing efficiency of transfer of polynucleotide into a target
PT      mammalian cell in vitro, involves exposing cell that expresses a stem
PT      cell factor receptor to stem cell factor, and introducing
PT      polynucleotide into cell in vitro -
XX
PS      Claim 17; Fig 42; 210pp; English.
XX
XX
CC      The present invention describes a method for enhancing (E) the
CC      efficiency of transfer of a polynucleotide (I) into a target mammalian
CC      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
CC      factor (SCF) receptor to a biologically active SCF, its analogue or
CC      fragment, which induces cell proliferation, and introducing (I) to (II)
CC      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
CC      into the cell. The method is useful for enhancing the efficiency of the
CC      transfer of a polynucleotide into a target mammalian cell in vitro.
CC      The method is useful in gene therapy techniques. AAH41301 to AAH41364
CC      and AAB98351 to AAB98390 represent sequences used in the exemplification
CC      of the present invention.
XX
XX
SQ      Sequence 273 AA.

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Query Match      100.0%; Score 1397; DB 22; Length 273;
Best local Similarity 100.0%; Pred. No. 2,8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MKKTGWIILCTYLOLLLEPVLKTEGICRNRTNNVAVTKLVANLPRDWMITLKYPG 60
        |||

```

```

Db      1 mktqwtlltctyqlllfnplvkktegiicrrvrenvkvdkvlvanlpkdymltkyvp 60
QY      61 MDVLPSCWISDMVYQSLDSTLTDLDFKFSNISELSNWTSTDKLYNVVDLVECVKENS 120
Db      61 mdtvlpshcwisemvqvslsdsltdkfsniseqlsnwtstdklynvvdldvecvkens 120
QY      121 KDIKSFKSPPEPLTPEPEFRIFENRSIDAFKDVVASETSDCVVSSTLSPKDSRVSVT 180
Db      121 KdIKSFkSpEplTtPeEfrIFeNRSIdAFKdVvASeTSdCVvSStLSPeKdSRvSVt 180
QY      181 KEFMLPYVAASSLRNDSSSNRKAKNPQDSSLHWAMALPALSLIIGFAGLYWKKR 240
Db      181 kpfmlppvaasslrndsssnrkaknpqgsslhwaamalpalflsligfagalywkkrr 240
QY      241 QPSLTRAVENIQINEEDNEISMLOEKEREPOEV 273
Db      241 qpsltraveniqineedneismloekerefev 273

RESULT 9
AAU02460
ID      AAU02460 standard; Protein; 273 AA.
XX
AC      AAU02460;
XX
DE      29-AUG-2001 (first entry)
XX
DE      Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
KW      Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW      HT1080 fibrosarcoma.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Protein      Location/Qualifiers
FT      Protein      1..25
FT      Protein      /label= Signal_peptide
FT      Protein      26..273
FT      Protein      /label= Mature_SCF
XX
PN      US6207417-B1.
XX
PD      27-MAR-2001.
XX
PE      07-JUN-1995; 95US-0482918.
XX
PR      21-DEC-1993; 93US-0172329.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
XX
PA      (ZSEBO/) ZSEBO K M.
PA      (BOSS/) BOSSELMAN R A.
PA      (SUGG/) SUGGS S V.
PA      (MART/) MARTIN F H.
XX
PI      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR      WPI; 2001-298941/31.
DR      N-PSDB; AAS04124.
XX
XX
PT      Novel nucleic acids encoding stem cell factor useful for treating
PT      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
PT      disease, kala azar, anaemia and septicemia -
XX
XX
PS      Example 5; Fig 42A-42C; 209pp; English.
XX
XX
CC      The present sequence representing human SCF (stem cell factor) protein
CC      is isolated from the HT1080 fibrosarcoma cell line. The present invention
CC      relates to novel stem cell factors (AAU02453-AAU02458, AAU02461) and

```

CC the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 XX
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLFPNLYKTEGICRNRVTNNKDYTKLVANIPKRYMTTLKYVPG 60
 Db 1 mktqtwtllctiyqlllfnplvktegicrnrvtnnvkdytklvaniplkrymttlkyvpg 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 mdvlpshcwissemvqslsdslldkfsniseglsnysiidklvniydvdlveckekenss 120
 QY 121 KDILKSKSPSPRLFTPEEFERIFNRSIDAFKDFVVASETSDCVSSSTLSPEKDSRVSVT 180
 Db 121 kdilkskspsprrlftpeeffrfrfnrsidafkdfvvasetsdcvssstlspekdsrvsvt 180
 QY 181 KPFLMPVPAASSLRNDSSSNRRKKNPPGSSLSHMAAMALPALFSLITIGAFGALYWKRR 240
 Db 181 kpflmpvpaasslrndsssnrrkknppgsslhmaamalpalfsliitgafgalywkr 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 qpsltraveniqineedneismleqekerefev 273

RESULT 10
 AAU02766 .
 ID AAU02766 standard; Protein; 273 AA.

AC AAU02766;
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW HT1080 fibrosarcoma.
 XX
 OS Homo sapiens.

EH Key Location/Qualifiers
 FT Protein 1..25
 FT /label= Signal_peptide
 FT Protein 26..273
 FT /label= Mature_SCF

XX US6218148-B1.
 XX 17-APR-2001.
 XX
 XX 21-DEC-1993; 93US-0172329.
 XX
 XX 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.

PI Zsebo KM, Bossejman RA, Suggs SV, Martin FH;
 XX WPI; 2001-281051/29.
 DR N-PSDB; AAS04224.
 XX

PT Isolated DNA sequence, encoding polypeptide product useful for
 PT stimulating growth of early haematopoietic progenitor cells -
 XX
 XX Example 5; Fig 42A-42C; 167pp; English.

XX The present sequence representing human SCF (stem cell factor) protein
 CC is isolated from the HT1080 fibrosarcoma cell line. The present
 CC invention relates to novel stem cell factors
 CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04218) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 XX
 XX Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLFPNLYKTEGICRNRVTNNKDYTKLVANIPKRYMTTLKYVPG 60
 Db 1 mktqtwtllctiyqlllfnplvktegicrnrvtnnvkdytklvaniplkrymttlkyvpg 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 mdvlpshcwissemvqslsdslldkfsniseglsnysiidklvniydvdlveckekenss 120
 QY 121 KDILKSKSPSPRLFTPEEFERIFNRSIDAFKDFVVASETSDCVSSSTLSPEKDSRVSVT 180
 Db 121 kdilkskspsprrlftpeeffrfrfnrsidafkdfvvasetsdcvssstlspekdsrvsvt 180
 QY 181 KPFLMPVPAASSLRNDSSSNRRKKNPPGSSLSHMAAMALPALFSLITIGAFGALYWKRR 240
 Db 181 kpflmpvpaasslrndsssnrrkknppgsslhmaamalpalfsliitgafgalywkr 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 qpsltraveniqineedneismleqekerefev 273

RESULT 11
 AAB73567
 ID AAB73567 standard; Protein; 273 AA.

AC AAB73567;
 DT 07-AUG-2001 (first entry)
 XX

DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFPNPKVTGICRNRYTNVKKDYTKLVANLPKDYMITLKYPG 60
 DB 1 mkkqtwlltcylyqlllfnplvkegicrnrvtnnvkdytklvannlpkdymitlkypg 60

QY 61 MDVLPSCWISSEMYVOLSDSLTDLLDKFSNISSEGLSNYSIIDKLNVNVDLVCEVKENSS 120
 DB 61 mdvlpshcwissemvqslsdsltdlldkfsnisseglsnysiidklvnvdllvecvkenss 120

QY 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 kdlkksfkspeprlftpeeffrrifnrsidafkdfvvasetsdcvvsstlspekdsrvsvt 180

QY 181 KPEMLPVAASSLRNDSSSNRKAKNPBGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 DB 181 kpfmlpvaasslrndsssnrkaknpbgdsslhmaamalpalfslllgfagalywkr 240

QY 241 QPSLTRAIVENIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismloekerefgev 273

RESULT 13

AAB96942
 ID AAB96942 standard; Protein: 273 AA.

XX AAB96942;

DT 13-JUL-2001 (first entry)

DE Human stem cell factor SEQ ID NO: 49.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;

KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;

KM neurological damage; intestinal damage; infertility; AIDS; SCID;

XX severe combined immunodeficiency.

OS Homo sapiens.

XX US6207802-B1.

PN 27-MAR-2001.

XX 09-NOV-1994; 94US-0336728.

XX 25-NOV-1992; 92US-0982255.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI: 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide

CC stimulating growth of early haematopoietic progenitor cells; useful for

CC treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,

XX sarcoidosis -

XX Example 3; Fig 16; 209pp; English.

CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is an SCF described in the
 CC invention.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFPNPKVTGICRNRYTNVKKDYTKLVANLPKDYMITLKYPG 60
 DB 1 mkkqtwlltcylyqlllfnplvkegicrnrvtnnvkdytklvannlpkdymitlkypg 60

QY 61 MDVLPSCWISSEMYVOLSDSLTDLLDKFSNISSEGLSNYSIIDKLNVNVDLVCEVKENSS 120
 DB 61 mdvlpshcwissemvqslsdsltdlldkfsnisseglsnysiidklvnvdllvecvkenss 120

QY 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 kdlkksfkspeprlftpeeffrrifnrsidafkdfvvasetsdcvvsstlspekdsrvsvt 180

QY 181 KPEMLPVAASSLRNDSSSNRKAKNPBGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 DB 181 kpfmlpvaasslrndsssnrkaknpbgdsslhmaamalpalfslllgfagalywkr 240

QY 241 QPSLTRAIVENIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismloekerefgev 273

RESULT 14

AAB96952
 ID AAB96952 standard; Protein: 273 AA.

XX AAB96952;

DT 13-JUL-2001 (first entry)

DE Human stem cell factor SEQ ID NO: 61.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;

KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;

KM neurological damage; intestinal damage; infertility; AIDS; SCID;

XX severe combined immunodeficiency.

OS Homo sapiens.

XX Key

FT Peptide

FT Protein

FT /label= mature_stem_cell_factor

XX US6207802-B1.

PN 27-MAR-2001.

XX 09-NOV-1994; 94US-0336728.

XX 25-NOV-1992; 92US-0982255.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI: 2001-353108/37.

DR N-PSDB; AAF89104.

```

XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early haematopoietic progenitor cells, useful for
PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis -
XX
PS Example 3; Fig 42; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is an SCF described in the
CC invention.
CC
XX
SQ Sequence 273 AA;
Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKQTWILTCIYQLILFNPVLTKEGICRNRYTNVKKDVTKLVANLPKDYMITLKYPG 60
DB 1 mkkqtwtllctylqllfnpvltkegicrnrvtmkkdvtklvannlpkdymitlkypg 60
QY 61 MDVLPSCHWISEMVOVLSDSLTDLDKFSNISSEGLSNYSIDKLVNIYDDIVECKENSS 120
DB 61 mdvlpshcwisemvovlsdsltdldkfsnisseglsnysidklvniyddiveckenss 120
QY 121 KDILKSKSPSPRLFTPEEPFRIFNRSIDAFKDVVASSETSDCVVSSSTLSPKDSRVSVT 180
DB 121 kdilkskspsprlftpeepfrifnrnsidafkdvvasetsdsvsstlspekdsrvsvt 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 kpflmpvaasslrndsssnrkaknpbgdssllhmaamalpalfsliigfagalwykkr 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 qpsltraveniqineedneismloekerefev 273
RESULT 15
AAU05256
ID AAU05256 standard; Protein; 273 AA.
XX
AC AAU05256;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human stem cell factor (SCF) protein encoded by SCF gene.
XX
KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; AIDS.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..25
FH Protein /label= Signal_peptide
FT 26..273
FT /label= Mature_SCF
XX
XX US6248319-B1.
XX 19-JUN-2001.
XX
XX 24-MAY-1995; 95US-0449653.

```

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XX
PR 10-APR-1991; 91US-0684535.
PR 25-NOV-1992; 92US-0988225.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 01-OCT-1990; 90US-0589701.
PR 21-DEC-1993; 93US-0172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI, 2001-407312/43.
DR N-PSDB; AAS10458.
XX
PT Increasing the number of early haematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell
PT factor -
XX
PS Example 3; Fig 15D; 210pp; English.
XX
CC The present sequence represents human stem cell factor (SCF) protein
CC encoded by the SCF gene. The sequence is described in an invention
CC relating to novel stem cell factors, the polynucleotides encoding them
CC and methods for producing the stem cell factors. The methods involve
CC increasing the number of early haematopoietic progenitor cells in human
CC peripheral blood by administering a haematopoietically effective human
CC stem cell factor polypeptide. The methods are useful for the treatment
CC of blood disorders, including myelofibrosis, myelodysplasia,
CC osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC refractory anaemia, malaria, vitamin B12 and folic acid deficiency,
CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
CC including AIDS.
XX
SQ Sequence 273 AA;
Query Match 99.6%; Score 1392; DB 22; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.1e-133;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKQTWILTCIYQLILFNPVLTKEGICRNRYTNVKKDVTKLVANLPKDYMITLKYPG 60
DB 1 mkkqtwtllctylqllfnpvltkegicrnrvtmkkdvtklvannlpkdymitlkypg 60
QY 61 MDVLPSCHWISEMVOVLSDSLTDLDKFSNISSEGLSNYSIDKLVNIYDDIVECKENSS 120
DB 61 mdvlpshcwisemvovlsdsltdldkfsnisseglsnysidklvniyddiveckenss 120
QY 121 KDILKSKSPSPRLFTPEEPFRIFNRSIDAFKDVVASSETSDCVVSSSTLSPKDSRVSVT 180
DB 121 kdilkskspsprlftpeepfrifnrnsidafkdvvasetsdsvsstlspekdsrvsvt 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 kpflmpvaasslrndsssnrkaknpbgdssllhmaamalpalfsliigfagalwykkr 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 qpsltraveniqineedneismloekerefev 273

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Search completed: August 18, 2002, 13:08:02
 Job time: 407 sec

Sun Aug 18 14:09:03 2002

us-09-604-325a-61.rag

Page 11

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:04:01 ; Search time 41.62 Seconds

(without alignments)
160.216 Million cell updates/sec

Title: US-09-604-325A-61

Perfect score: 1397

Sequence: 1 MKKTQTWILTCIYLQLLFN.....NEEDNEISMLQEKERKQEV 273

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	1	US-08-220-379B-2
2	1397	100.0	273	2	US-08-628-428-9
3	1397	100.0	273	4	US-08-482-918-49
4	1397	100.0	273	4	US-08-482-918-61
5	1397	100.0	273	4	US-09-224-681-49
6	1397	100.0	273	4	US-09-224-681-61
7	1397	100.0	273	4	US-08-336-728A-48
8	1397	100.0	273	4	US-08-336-728A-49
9	1397	100.0	273	4	US-08-336-728A-61
10	1397	99.6	273	4	US-08-482-918-48
11	1397	99.6	273	4	US-09-224-681-48
12	1381	98.9	273	4	US-08-482-918-50
13	1381	98.9	273	4	US-09-224-681-50
14	1378	98.6	273	4	US-08-336-728A-50
15	1265	90.6	248	2	US-08-955-848A-82
16	1232.5	88.2	266	4	US-08-482-918-57
17	1232.5	88.2	266	4	US-09-224-681-57
18	1232.5	88.2	266	4	US-08-336-728A-57
19	1231	88.1	245	4	US-08-482-918-63
20	1231	88.1	245	4	US-09-224-681-63
21	1231	88.1	245	4	US-08-336-728A-63
22	1202.5	86.1	274	4	US-08-482-918-51
23	1180.5	84.5	274	4	US-09-224-681-51
24	1180.5	84.5	274	4	US-08-336-728A-51
25	1179.5	84.4	271	4	US-08-482-918-52
26	1179.5	84.4	271	4	US-09-224-681-52
27	1179.5	84.4	271	4	US-08-336-728A-52

28	1178.5	84.4	274	4	US-08-336-728A-53	Sequence 53, Appl
29	1173	84.0	273	4	US-08-482-918-53	Sequence 53, Appl
30	1173	84.0	273	4	US-09-224-681-53	Sequence 53, Appl
31	1158	82.9	273	4	US-08-482-918-42	Sequence 42, Appl
32	1158	82.9	273	4	US-09-224-681-42	Sequence 42, Appl
33	1158	82.9	273	4	US-08-336-728A-42	Sequence 54, Appl
34	1158	82.9	273	4	US-08-336-728A-54	Sequence 54, Appl
35	1157	82.8	273	1	US-08-220-379B-6	Sequence 55, Appl
36	1157	82.8	273	4	US-08-482-918-55	Sequence 55, Appl
37	1157	82.8	273	4	US-09-224-681-55	Sequence 55, Appl
38	1157	82.8	273	4	US-08-336-728A-55	Sequence 55, Appl
39	1151	82.4	273	4	US-08-482-918-54	Sequence 54, Appl
40	1151	82.4	273	1	US-09-224-681-54	Sequence 54, Appl
41	1144	81.9	273	4	US-08-336-728A-11	Sequence 11, Appl
42	1144	81.9	273	3	US-08-478-414A-11	Sequence 11, Appl
43	1144	81.9	273	3	US-08-325-240A-11	Sequence 11, Appl
44	1144	81.9	273	4	US-08-898-982-11	Sequence 11, Appl
45	1030	73.7	208	4	US-08-836-252A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-220-379B-2
; Sequence 2, Application US/08220379B
; Patent No. 5525708
; GENERAL INFORMATION:
; APPLICANT: No. 5525708Ka, Karl
; APPLICANT: Lobell, Robert B
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,379B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytomed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: cleavage site
; LOCATION: 164..165
; US-08-220-379B-2

Query Match 100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKKTQTWILTCIYLQLLFNVLVTEGICRRRTYNNKVDYTKLVANIPKDYMTTKYVGC 60
|||||

Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
QY 121 KDLKSKSEKPEPRFLTPPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDLKSKSEKPEPRFLTPPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSNSSNRKAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
Db 181 KPEMLPVAASSLRNDSNSSNRKAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 2

US-08-628-428-9
; Sequence 9, Application US/08628428
; Patent No. 5885962
; GENERAL INFORMATION:
; APPLICANT: Lu, Hsieng
; TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,428
; FILING DATE: 05-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..273
; OTHER INFORMATION: /note="NOTE: Mature full length
; OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
; OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
; OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 100.0%; Score 1397; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKDYTKLVANLPKDYMITLKYPG 60
Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120

Db 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
QY 121 KDLKSKSEKPEPRFLTPPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDLKSKSEKPEPRFLTPPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSNSSNRKAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
Db 181 KPEMLPVAASSLRNDSNSSNRKAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 3

US-08-482-918-49
; Sequence 49, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Sugars, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-49

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKDYTKLVANLPKDYMITLKYPG 60
Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120

QY 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDPVVASETSDCVSSTLSPKDSRVSAT 180
DB 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDPVVASETSDCVSSTLSPKDSRVSAT 180
QY 181 KPFMLPVAASSLRNDSSSNRRKAKNPBGDSLHWAAMALPALFSLIGFAFGALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRRKAKNPBGDSLHWAAMALPALFSLIGFAFGALYWKRR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 4
US-08-482-918-61
Sequence 61, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 61:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-61

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2, 1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWLTCTCYIQLLFNPLVYKTEGICRNRVNNVAKDVKLVANLPRKDYMTLKYPVG 60
DB 1 MKKTQTWLTCTCYIQLLFNPLVYKTEGICRNRVNNVAKDVKLVANLPRKDYMTLKYPVG 60
QY 61 MDVLPSCWISSEMYVQLSDSLTDLDRKSNISEGINSYITDKLVNTVYDDIVEGVKKNSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLTDLDRKSNISEGINSYITDKLVNTVYDDIVEGVKKNSS 120
QY 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDPVVASETSDCVSSTLSPKDSRVSAT 180
DB 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFKDPVVASETSDCVSSTLSPKDSRVSAT 180

QY 181 KPFMLPVAASSLRNDSSSNRRKAKNPBGDSLHWAAMALPALFSLIGFAFGALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRRKAKNPBGDSLHWAAMALPALFSLIGFAFGALYWKRR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 5
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TRANSFER WITH STEM CELL FACTOR (SCF) POLYPEPTIDE
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRYNNVNDVTKLVANLPKDYMITLKYPG 60
DB 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRYNNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
DB 61 MDVLPSCWISSEMYVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
QY 121 KDLKSKSPSPRLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSITRAVENIQINEEDNEISMLQEKEREFOEV 273
DB 241 QPSITRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 6

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.

APPLICANT: Bosseiman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS: Transfer with Stem Cell Factor (SCF) Polypeptide

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,681

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/449,653

FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: 07/537,198
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRYNNVNDVTKLVANLPKDYMITLKYPG 60
DB 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRYNNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
DB 61 MDVLPSCWISSEMYVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
QY 121 KDLKSKSPSPRLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSITRAVENIQINEEDNEISMLQEKEREFOEV 273
DB 241 QPSITRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 7

US-08-336-728A-48

Sequence 48, Application US/08336728A

Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.

APPLICANT: Bosseiman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,728A
;; FILING DATE: 09-NOV-1994
;; CLASSIFICATION: 424
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/982,255
;; FILING DATE: 25-NOV-1992
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/589,701
;; FILING DATE: 01-OCT-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/573,616
;; FILING DATE: 24-AUG-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/537,198
;; FILING DATE: 11-JUN-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/422,383
;; FILING DATE: 16-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W.
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 01017/32956
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 1 MKKTOTWILTCIYIOLLFNPVKTGEGICRNVTNNVADVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYIOLLFNPVKTGEGICRNVTNNVADVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMVVQLSDSLDLDKFSNISEGLSNYSIIDKLVIIVDVLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQLSDSLDLDKFSNISEGLSNYSIIDKLVIIVDVLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSNRKAANPPGDDSLHMAAALPALFSLIIGFAFGALYMKKR 240
DB 181 KPMLPPVAASSLRNDSSSNRKAANPPGDDSLHMAAALPALFSLIIGFAFGALYMKKR 240
QY 241 OPSLTRAVENTIINEEDNEISMLOEKEREFOEV 273
DB 241 OPSLTRAVENTIINEEDNEISMLOEKEREFOEV 273

RESULT 8
US-08-336-728A-49
;; Sequence 49, Application US/0836728A
;; Patent No. 6207802
;; GENERAL INFORMATION:
;; APPLICANT: zsebo, Kristztina M.
;; APPLICANT: Bosseiman, Robert A.
;; APPLICANT: Suggs, Sidney V.
;; APPLICANT: Martin, Francis H.
;; TITLE OF INVENTION: Stem Cell Factor
;; NUMBER OF SEQUENCES: 104
;; CORRESPONDENCE ADDRESS:

;;
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,728A
;; FILING DATE: 09-NOV-1994
;; CLASSIFICATION: 424
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/982,255
;; FILING DATE: 25-NOV-1992
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/589,701
;; FILING DATE: 01-OCT-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/573,616
;; FILING DATE: 24-AUG-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/537,198
;; FILING DATE: 11-JUN-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/422,383
;; FILING DATE: 16-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W.
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 01017/32956
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 1 MKKTOTWILTCIYIOLLFNPVKTGEGICRNVTNNVADVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYIOLLFNPVKTGEGICRNVTNNVADVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMVVQLSDSLDLDKFSNISEGLSNYSIIDKLVIIVDVLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQLSDSLDLDKFSNISEGLSNYSIIDKLVIIVDVLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSNRKAANPPGDDSLHMAAALPALFSLIIGFAFGALYMKKR 240
DB 181 KPMLPPVAASSLRNDSSSNRKAANPPGDDSLHMAAALPALFSLIIGFAFGALYMKKR 240
QY 241 OPSLTRAVENTIINEEDNEISMLOEKEREFOEV 273
DB 241 OPSLTRAVENTIINEEDNEISMLOEKEREFOEV 273

RESULT 9
US-08-336-728A-61
; Sequence 61, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Kristzina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEO ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTOTWITTCIYLOLLFNPLVKTGICRNRVTNNVAVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTOTWITTCIYLOLLFNPLVKTGICRNRVTNNVAVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQVLSLFDLDFKFSNISBGLSNYSIIDKLVNIYDDIVECVKENS 120
DB 61 MDVLPSCWISSEMYVQVLSLFDLDFKFSNISBGLSNYSIIDKLVNIYDDIVECVKENS 120
QY 121 KDLKSKFSPEPRFLTPEEFRIFRNSIDAKDFVVASSETDCVVSSTLSEKRSRVS 180
DB 121 KDLKSKFSPEPRFLTPEEFRIFRNSIDAKDFVVASSETDCVVSSTLSEKRSRVS 180

DB 121 KDLKSKFSPEPRFLTPEEFRIFRNSIDAKDFVVASSETDCVVSSTLSEKRSRVS 180
QY 181 KPEMLPPVAASSLRDSSSSNRKAKNPPGDSLLHMAALPALFSLIIGFAGALYKKR 240
DB 181 KPEMLPPVAASSLRDSSSSNRKAKNPPGDSLLHMAALPALFSLIIGFAGALYKKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 10
US-08-482-918-48
; Sequence 48, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Kristzina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEO ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-48

Query Match 99.6%; Score 1392; DB 4; Length 273;
Best Local Similarity 99.6%; Pred. No. 6,6e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTOTWITTCIYLOLLFNPLVKTGICRNRVTNNVAVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTOTWITTCIYLOLLFNPLVKTGICRNRVTNNVAVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQVLSLFDLDFKFSNISBGLSNYSIIDKLVNIYDDIVECVKENS 120
DB 61 MDVLPSCWISSEMYVQVLSLFDLDFKFSNISBGLSNYSIIDKLVNIYDDIVECVKENS 120
QY 121 KDLKSKFSPEPRFLTPEEFRIFRNSIDAKDFVVASSETDCVVSSTLSEKRSRVS 180
DB 121 KDLKSKFSPEPRFLTPEEFRIFRNSIDAKDFVVASSETDCVVSSTLSEKRSRVS 180
QY 181 KPEMLPPVAASSLRDSSSSNRKAKNPPGDSLLHMAALPALFSLIIGFAGALYKKR 240
DB 181 KPEMLPPVAASSLRDSSSSNRKAKNPPGDSLLHMAALPALFSLIIGFAGALYKKR 240

Db 101 KPFMLPVAASSLRNDSSSSNRKAKNPPGSSSLHWPAMALPALFSLIIGFAGALYMKR 240
QY 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 11
US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 99.6%; Score 1392; DB 4; Length 273;
Best Local Similarity 99.6%; Pred. No. 6,6e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWIIITLCIYLQLLFNPLVKTGICRNRVTNNKQVTKLVANLPKDYMITLKYPG 60
Db 1 MKKTQWIIITLCIYLQLLFNPLVKTGICRNRVTNNKQVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISEMNVOLSDSLFDLDKFSNISEGLSNYSITDKLVNYDDIVECKENSS 120
Db 61 MDVLPSCWISEMNVOLSDSLFDLDKFSNISEGLSNYSITDKLVNYDDIVECKENSS 120
QY 121 KDLKSEFKSPPEPLTFPEEFRIFNRSIDAFKDPVVASSETSCVVSSTLSPKDSRVSVT 180
Db 121 KDLKSEFKSPPEPLTFPEEFRIFNRSIDAFKDPVVASSETSCVVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNRKAKNPPGSSSLHWPAMALPALFSLIIGFAGALYMKR 240
Db 181 KPFMLPVAASSLRNDSSSSNRKAKNPPGSSSLHWPAMALPALFSLIIGFAGALYMKR 240
QY 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 12
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 98.9%; Score 1381; DB 4; Length 273;

Best Local Similarity 98.9%; Pred. No. 8.8e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISSEGLSNSTIDKLVNIVDDLYECVKNSS 120
DB 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISSEGLSNSTIDKLVNIVDDLYECVKNSS 120
QY 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSEKDSRVSVT 180
DB 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGSSLHWAAMALPAFLSLIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGSSLHWAAMALPAFLSLIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOV 273

RESULT 13
US-09-224-681-50
Sequence 50, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: 104
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224, 681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005, 893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449, 653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982, 255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589, 701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573, 616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422, 383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36, 107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
SPRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-50

Query Match 98.9%; Score 1381; DB 4; Length 273;
Best Local Similarity 98.9%; Pred. No. 8.8e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISSEGLSNSTIDKLVNIVDDLYECVKNSS 120
DB 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISSEGLSNSTIDKLVNIVDDLYECVKNSS 120
QY 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSEKDSRVSVT 180
DB 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGSSLHWAAMALPAFLSLIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGSSLHWAAMALPAFLSLIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOV 273

RESULT 14
US-08-336-728A-50
Sequence 50, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336, 728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA: 07/589,701
APPLICATION NUMBER: 01-OCT-1990
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-50

Query Match 98.6%; Score 1378; DB 4; Length 273;
Best Local Similarity 98.5%; Pred. No. 1.8e-132;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWIICTCIYLOLLFNPLKTEGICRNVYNNKQVYTLVANLPKDYMITLKYYVG 60
DB 1 MKKTQWIICTCIYLOLLFNPLKTEGICRNVYNNKQVYTLVANLPKDYMITLKYYVG 60
QY 61 MDVLPSCHWISEMNVQVLSLTDLLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MDVLPSCHWISEMNVQVLSLTDLLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
QY 121 KDLKSKFKPEPRLTPTPEEFRIENKSIDAFKDFYVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSKFKPEPRLTPTPEEFRIENKSIDAFKDFYVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIQINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEDNEISMLOEKEREFOEV 273

RESULT 15
US-08-955-848A-82
Sequence 82, Application US/08955848A
Patent No. 5969105
GENERAL INFORMATION:
APPLICANT: Mc Welter, Charles
APPLICANT: Feng, Yiding
TITLE OF INVENTION: No. 5969105el Stem Cell Factor Receptor
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. D. Searle & Co.
STREET: P.O. Box 5110
CITY: Chicago
STATE: IL
COUNTRY: U. S. A.

ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955, 848A
FILING DATE: 21-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,165
FILING DATE: 25-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2992/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
TELEFAX: 314-737-6972
TELEX:
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-955-848A-82

Query Match 90.6%; Score 1265; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-121;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGICRNRVTNNKQVYTLVANLPKDYMITLKYYGMDVLPSCHWISEMNVQVLSLTDLL 85
DB 1 EGICRNRVTNNKQVYTLVANLPKDYMITLKYYGMDVLPSCHWISEMNVQVLSLTDLL 85
QY 86 DKFSNISEGLSNYSIIDKLVNIYDDIVECKENSSKDLKSKFKSPERLTPTPEEFRIFN 145
DB 61 DKFSNISEGLSNYSIIDKLVNIYDDIVECKENSSKDLKSKFKSPERLTPTPEEFRIFN 120
QY 146 RSIDAFKDFYVASETSDCVVSTLSPEKDSRVSVTKPFMLPVAASSLRNDSSSNRKAK 205
DB 121 RSIDAFKDFYVASETSDCVVSTLSPEKDSRVSVTKPFMLPVAASSLRNDSSSNRKAK 180
QY 206 NPQDSSLHMAAMALPALFSLIIGFAFGALYMKRQPSLTRAVENTIQINEDNEISMLOE 265
DB 181 NPQDSSLHMAAMALPALFSLIIGFAFGALYMKRQPSLTRAVENTIQINEDNEISMLOE 240
QY 266 KEREFOEV 273
DB 241 KEREFOEV 248

Search completed: August 18, 2002, 13:04:01
Job time: 166 sec

Sun Aug 18 14:09:03 2002

us-09-604-325a-61.rai

Page 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:03:13 ; Search time 62.73 Seconds

(without alignments)
418.179 Million cell updates/sec

Title: US-09-604-325a-61

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREFQEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	DB ID	Description
1	1397	100.0	273	2	A35974	most cell growth f
2	1231	88.1	245	2	B61190	most cell growth f
3	1203.5	86.1	274	2	I46575	c-kit ligand - pig
4	1184.5	84.8	274	2	S47571	stem cell factor,
5	1180.5	84.5	274	2	I46929	stem cell factor,
6	1157	82.8	273	2	S65801	stem cell factor,
7	991	70.9	245	2	A37934	stem cell growth f
8	885.5	63.4	202	2	S58313	stem cell growth f
9	857	61.3	201	2	B35974	stem cell factor p
10	703	50.3	287	2	JN0637	stem cell factor p
11	702	50.3	287	2	S70367	stem cell factor p
12	589	42.2	253	2	S70367	stem cell factor 1
13	576.5	41.3	124	2	S29052	stem cell factor s
14	175.5	12.6	51	2	B35971	stem cell growth f
15	172.5	12.3	49	2	A35971	stem cell growth f
16	106	7.6	465	2	H97165	flagellar hook-len
17	101	7.2	1490	2	T16086	hypothetical prote
18	100.5	7.2	402	2	T09062	hypothetical prote
19	100.5	7.2	647	2	F90595	probable advanced
20	97.5	7.0	1107	2	S61667	conserved hypochet
21	97	6.9	1447	2	F82909	probable membrane
22	95.5	6.8	484	2	T25944	hypothetical prote
23	95.5	6.8	614	2	B86461	hypothetical prote
24	93.5	6.7	1293	2	T27886	probable protein k
25	93.5	6.7	1813	2	T19295	hypothetical prote
26	92.5	6.6	164	2	B69616	hypothetical prote
27	92.5	6.6	246	2	T19850	cell-division init
28	92.5	6.6	398	2	I53340	hypothetical prote
29	92.5	6.6	512	2	G86773	paired box transcr
						citrate (pro-35)-1

ALIGNMENTS

Query Match	Best Local Similarity	100.0%	Score 1397	DB 2	Length 273	Pred. No. 5.8e-103	Mismatches 0	Indels 0	Gaps 0
Matches 273	Conservative	0	Mismatches	0	Indels	0	Gaps	0	
QY	1	MKKTQWILTCIYLQLLFNPLVTEGICGRNRYNNVWKDVTKLVANLPKDYMITLKYVG	60						
DB	1	MKKTQWILTCIYLQLLFNPLVTEGICGRNRYNNVWKDVTKLVANLPKDYMITLKYVG	60						
QY	61	MDVLPSHCWISSENVVQSLDLDLKFNSISEGLSNYSIIDKLVIYVDLVECKENSS	120						
DB	61	MDVLPSHCWISSENVVQSLDLDLKFNSISEGLSNYSIIDKLVIYVDLVECKENSS	120						
QY	121	KDKKSFKSPPEPLFPPEEPFRIFNRSIDAFKDFVVASETSCVVSSTLSPKDSRVST	180						
DB	121	KDKKSFKSPPEPLFPPEEPFRIFNRSIDAFKDFVVASETSCVVSSTLSPKDSRVST	180						

RESULT 5
146929
C:Species: Canis lupus familiaris (dog)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: 146929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic F
A:Reference number: 146929; MUID:93106145
A:Accession: 146929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
A:Cross-references: GB:S53329; NID:g262240; PIDN:AA24619.1; PID:g262241
C:Superfamily: mouse mast cell growth factor

Query Match 84.5%; Score 1180.5; DB 2; Length 274;
Best Local Similarity 85.4%; Pred. No. 7.3e-86;
Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

OY 1 MKKTQTWITTCYIQLLLFNPVTEGICRRRVNNKADVTKLVANLPKDYMTLKYPG 60
DB 1 MKKTQTWITTCYIQLLLFNPVTEGICRRRVNNKADVTKLVANLPKDYMTLKYPG 60
OY 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISEGNSYIIDKLVNIVDDVECKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISEGNSYIIDKLVNIVDDVECKENSS 120
OY 121 KDLKSEKSPERLFTPEEFRIINRSIDAKDF-VVASETSDCVSSTLSPKDSRSV 179
DB 121 ENVKAPKSPERLFTPEEFRIINRSIDAKDF-VVASETSDCVSSTLSPKDSRSV 180
OY 180 TKPFLPVAASLRNDSNRKAKPPGDSLSHMAALPALFSLIGFAGALYWK 239
DB 181 TKPFLPVAASLRNDSNRKAKPPGDSLSHMAALPALFSLIGFAGALYWK 240
OY 240 KQPSLTRAVENIQINEDNEISMLOEKERPEOV 273
DB 241 KQPSLTRAVENIQINEDNEISMLOEKERPEOV 274

RESULT 6
563801
mast cell growth factor - mouse
N:Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
C:Accession: S65801; A43751; A35976; A35977; A35972; A35975; A35973; I48768
R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A:Title: Multiple pathways for steel regulation suggested by genomic and sequence analysis
A:Reference number: S65801; MUID:97002551
A:Accession: S65801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <BED>
A:Cross-references: EMBL:U44725; NID:g1172215; PIDN:AA25447.1; PID:g1172216
R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the kit-
A:Reference number: A43751; MUID:92330001
A:Accession: A43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-214, 'V', 216-273 <HUA>
A:Cross-references: GB:S40364; NID:g251668; PIDN:AA22554.2; PID:g5705957
R:Huang, E.; Nocka, K.; Beter, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
Cell 63, 225-233, 1990

A:Title: The hematopoietic growth factor KL is encoded by the S1 locus and is the lig
A:Reference number: A35976; MUID:91004221
A:Accession: A35976
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-206, 'S', 208-270 <HU2>
A:Cross-references: GB:M38511
R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; Mar
Cell 63, 235-243, 1990
A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active
A:Reference number: A35977; MUID:91004223
A:Accession: A35977
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Cross-references: GB:M57647; GB:M38436; NID:g199151; PIDN:AA39538.1; PID:g199152
R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.;
Cell 63, 175-183, 1990
A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and
A:Reference number: A35972; MUID:91004216
A:Accession: A35972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 26-53 <COP>
A:Cross-references: GB:M59912
R:Sebo, K.M.; Williams, D.A.; Geissler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.
Cell 63, 213-224, 1990
A:Title: Stem cell factor is encoded at the S1 locus of the mouse and is the ligand f
A:Reference number: A35975; MUID:91004220
A:Accession: A35975
A:Molecule type: mRNA
A:Residues: 1-201 <ZSE>
A:Cross-references: GB:M59915; NID:g200935; PIDN:AAA40095.1; PID:g554271
R:Sebo, K.M.; Wypych, J.; Moniece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachd
Cell 63, 195-201, 1990
A:Title: Identification, purification, and biological characterization of hematopoiet
A:Reference number: A35973; MUID:91004218
A:Accession: A35973
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-29, 'R', 31-39 <ZS2>
R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.
Genes Dev. 6, 1832-1842, 1992
A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect 1
A:Reference number: A44071; MUID:93012940
A:Accession: A44071
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206, 'S', 208-273 <RES>
A:Cross-references: EMBL:X68989; NID:g395283; PIDN:CAA48778.1; PID:g395284
C:Genetics:
A:Gene: SLF
A:Map position: 10
C:Superfamily: mouse mast cell growth factor
C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 82.8%; Score 1157; DB 2; Length 273;
Best Local Similarity 82.8%; Pred. No. 5.2e-84;
Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

OY 1 MKKTQTWITTCYIQLLLFNPVTEGICRRRVNNKADVTKLVANLPKDYMTLKYPG 60
DB 1 MKKTQTWITTCYIQLLLFNPVTEGICRRRVNNKADVTKLVANLPKDYMTLKYPG 60
OY 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISEGNSYIIDKLVNIVDDVECKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISEGNSYIIDKLVNIVDDVECKENSS 120
OY 121 KDLKSEKSPERLFTPEEFRIINRSIDAKDF-VVASETSDCVSSTLSPKDSRSV 180
DB 121 KDLKSEKSPERLFTPEEFRIINRSIDAKDF-VVASETSDCVSSTLSPKDSRSV 180

Db 121 KNKESPKRPTTRSTTPEEFISINFRSIDAFAKDEWASDTSDCVLSSTLGPCKDSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSSNNKAKNPDPGSSLSHWAAMALPALPSLITGFAFGALYWKRR 240
 Db 181 KPFMLPPVAASSLRNDSSSSNNKAKNPDPGSSLSHWAAMALPALPSLITGFAFGALYWKRR 240
 QY 241 OPSLTRAVENTIOINEDNEISMLOEKERPEQEV 273
 Db 241 OPSLTRAVENTIOINEDNEISMLOEKERPEQEV 273

RESULT 7

mest cell growth factor precursor (version 2) - mouse

N:Alternative names: KL-2 protein

C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000

C:Accession: A37934; B43751

R:Flanagan, J.G.; Chan, D.C.; Leder, P.

Cell 64, 1025-1035, 1991

A:Title: Transmembrane form of the kit ligand growth factor is determined by alternative

A:Reference number: A37934; MUID:91160046

A:Accession: A37934

A:Molecule type: mRNA

A:Residues: 1-245 <FLA>

A:Cross-references: GB:M64262

R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.

Mol. Biol. Cell 3, 349-362, 1992

A:Title: Differential expression and processing of two cell associated forms of the kit-

A:Reference number: A43751; MUID:92330001

A:Accession: B43751

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-173, 'R', '175-186, 'L', '188-245 <HWA>

A:Cross-references: GB:S04534

A:Note: the authors translated the codon TTG for residue 187 as Trp

C:Superfamily: mouse mast cell growth factor

Query Match

Best local similarity 70.9%; Score 991; DB 2; Length 245;

Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVPG 60
 Db 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVAG 60
 QY 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
 Db 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
 QY 121 KNKESKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 174
 Db 121 KNKESKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 174
 QY 181 KPFMLPPVAASSLRNDSSSSNNKAKNPDPGSSLSHWAAMALPALPSLITGFAFGALYWKRR 240
 Db 181 KPFMLPPVAASSLRNDSSSSNNKAKNPDPGSSLSHWAAMALPALPSLITGFAFGALYWKRR 240
 QY 175 -----KAAPEDSGIOWTAMALPALISIVIGFAGALYWKRR 212
 Db 175 -----KAAPEDSGIOWTAMALPALISIVIGFAGALYWKRR 212
 QY 241 OPSLTRAVENTIOINEDNEISMLOEKERPEQEV 273
 Db 241 OPSLTRAVENTIOINEDNEISMLOEKERPEQEV 273

RESULT 8

stem cell factor precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000

C:Accession: S58313

R:Minnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.

submitted to the EMBL Data Library, August 1995

A:Description: Molecular cloning and biological activity of ovine stem cell factor.

A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:250743; NID:940807; PIDN:CAA90620.1; PID:940808
 C:Superfamily: mouse mast cell growth factor

Query Match

Best local similarity 63.4%; Score 885.5; DB 2; Length 202;

Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVPG 60
 Db 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVAG 60
 QY 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSV 179
 Db 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSV 180
 QY 180 TKPMLPPVAASSLRNDSSSSN 201
 Db 181 TKPMLPPVAASSLRNDSSSSN 202

RESULT 9

stem cell factor protein precursor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: B35974; A39805

R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, S.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, Cell 63, 203-211, 1990

A:Title: Primary structure and functional expression of rat and human stem cell facto

A:Reference number: A35974; MUID:91004219

A:Accession: B35974

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-201 <MAR>

A:Cross-references: GB:M59966; NID:920661; PIDN:AAA2117.1; PID:9554507

R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zse J. Biol. Chem. 266, 8102-8107, 1991

A:Title: Amino acid sequence and post-translational modification of stem cell factor

A:Reference number: A39805; MUID:91217037

A:Accession: A39805

A:Status: preliminary

A:Molecule type: protein

A:Residues: 'E', '27-190 <LUA>

C:Superfamily: mouse mast cell growth factor

Query Match

Best local similarity 61.3%; Score 857; DB 2; Length 201;

Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVPG 60
 Db 1 MKKTQWTLTCTIYQLLFPNPLVKTGICRNRYNNVAVKLVANLPKDYITTKYVAG 60
 QY 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIIDLKIVYIDDLVECVKENS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
 Db 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
 QY 121 KNKESKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180
 Db 121 KNKESKSPSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVVSSSTLSPKDSRVSVT 180

QY 181 KPEMLPVAASSLRNDSSSSN 201
 |||||
 Db 181 KPEMLPVAASSLRNDSSSSN 201

RESULT 10

stem cell factor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
 R:Zhou, J.H.; Ohtaki, M.; Sakurai, M.
 Gene 127, 266-270, 1993

A:Title: Sequence of a cDNA encoding chicken stem cell factor.
 A:Reference number: JN0637; MUID:93273244
 A:Accession: JN0637

A:Molecule type: mRNA
 A:Residues: 1-287 <ZHO>
 A:Cross-references: GB:D13516; NID:g391648; PIDN:BAA0273.1; PID:g391649
 A:Experimental source: brain
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor #status predicted <MAT>
 F:226-246/Domain: transmembrane #status predicted <TM>

Query Match 50.3%; Score 703; DB 2; Length 287;
 Best Local Similarity 51.9%; Pred. No. 4.1e-48;

Matches 149; Conservative 50; Mismatches 74; Indels 14; Gaps 6;

QY 1 MKKTQWILTCIYQLLEFNPVTEGICRNKRVNNVADVTKLVANLPKDYMTLKYPG 60
 |||||
 Db 1 MKKAQTWITTCFCLQLLLNPLVKAQSSCGNPYTDVDVNDIAKLVGNLPNDYLTITKYPK 60
 |||||
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNT---SEGLSNSTIIDKLVNIDVLECYKE 117
 |||||
 Db 61 MDLSLPNHCWLMWPEFSRSLHNLQKFSDISDMSDVLSNIIINLRIINDIMACIAF 120
 |||||
 QY 118 NSSKD-LKSKFSPERPLFPEEFRIENRSIDAFKDVVAASETSDCVVSTL-SPKDS 175
 |||||
 Db 121 DKNDFIKENHLYEDRFIPENFRNLNTEYKKEFADSLKNDICIMPSTVETPEPDS 180
 |||||
 QY 176 RVSATKPEMLPVAASSLRND-----SSSSNRKAKNPDDGSSLHMAALPALFSLIIG 229
 |||||
 Db 181 RVAVTKTISFPVAASSLRNDISGNTSSNSNKEALGFISSSLOGISIALTSLIIG 240
 |||||
 QY 230 FAFGALYKKRROP-SLTRAVENTIOIN--EEDNEISMLOEKEREFOEV 273
 |||||
 Db 241 FILGVIYKKTKHPKSPESNETTQCHGCOEENEISMLOEKEREHLQV 287
 |||||

RESULT 11
 stem cell factor long form precursor - quail

C:Species: Coturnix coturnix (quail)
 C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70366

R:Petitje, J.N.; Kulik, M.J.

Biochim. Biophys. Acta 1307, 149-151, 1996

A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac

A:Reference number: S70366; MUID:96283808
 A:Accession: S70366
 A:Molecule type: mRNA
 A:Residues: 1-287 <PPT>
 A:Cross-references: EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; PID:g1150876
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor long form #status predicted <MAT>
 F:226-250/Domain: transmembrane #status predicted <TM>

Query Match 50.3%; Score 702; DB 2; Length 287;
 Best Local Similarity 51.6%; Pred. No. 4.9e-48;
 Matches 148; Conservative 51; Mismatches 74; Indels 14; Gaps 6;

QY 1 MKKTQWILTCIYQLLEFNPVTEGICRNKRVNNVADVTKLVANLPKDYMTLKYPG 60
 |||||
 Db 1 MKKAQTWITTCFCLQLLLNPLVKAQSSCGNPYTDVDVNDIAKLVGNLPNDYLTITKYPK 60
 |||||
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNT---SEGLSNSTIIDKLVNIDVLECYKE 117
 |||||
 Db 61 MDLSLPNHCWLMWPEFSRSLHNLQKFSDISDMSDVLSNIIINLRIINDIMACIAF 120
 |||||
 QY 118 NSSKD-LKSKFSPERPLFPEEFRIENRSIDAFKDVVAASETSDCVVSTL-SPKDS 175
 |||||
 Db 121 DKNDFIKENHLYEDRFIPENFRNLNTEYKKEFADSLKNDICIMPSTVETPEPDS 180
 |||||
 QY 176 RVSATKPEMLPVAASSLRND-----SSSSNRKAKNPDDGSSLHMAALPALFSLIIG 229
 |||||
 Db 181 RVAVTKTISFPVAASSLRNDISGNTSSNSNKEALGFISSSLOGISIALTSLIIG 240
 |||||
 QY 230 FAFGALYKKRROP-SLTRAVENTIOIN--EEDNEISMLOEKEREFOEV 273
 |||||
 Db 241 FILGVIYKKTKHPKSPESNETTQCHGCOEENEISMLOEKEREHLQV 287
 |||||

RESULT 12

stem cell factor short form precursor - quail

C:Species: Coturnix coturnix (quail)
 C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70367

R:Petitje, J.N.; Kulik, M.J.

Biochim. Biophys. Acta 1307, 149-151, 1996

A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell

A:Reference number: S70366; MUID:96283808
 A:Accession: S70367
 A:Molecule type: mRNA
 A:Residues: 1-253 <PPT>
 A:Cross-references: EMBL:U43079; NID:g1150877; PIDN:AAC59934.1; PID:g1150878
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-253/Product: stem cell factor short form #status predicted <MAT>
 F:192-216/Domain: transmembrane #status predicted <TM>

Query Match 42.2%; Score 589; DB 2; Length 253;
 Best Local Similarity 45.2%; Pred. No. 3.5e-39;
 Matches 127; Conservative 48; Mismatches 70; Indels 36; Gaps 6;

QY 1 MKKTQWILTCIYQLLEFNPVTEGICRNKRVNNVADVTKLVANLPKDYMTLKYPG 60
 |||||
 Db 1 MKKAQTWITTCFCLQLLLNPLVKAQSSCGNPYTDVDVNDIAKLVGNLPNDYLTITKYPK 60
 |||||
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNT---SNISGLSNSTIIDKLVNIDVLECYKE 117
 |||||
 Db 61 MDLSLPNHCWLMWPEFSRSLHNLQKFSDISDMSDVLSNIIINLRIINDIMACIAF 120
 |||||
 QY 118 NSSKD-LKSKFSPERPLFPEEFRIENRSIDAFKDVVAASETSDCVVSTL-SPKDS 175
 |||||
 Db 121 DKNDFIKENHLYEDRFIPENFRNLNTEYKKEFADSLKNDICIMPSTVETPEPDS 177
 |||||
 QY 176 RVSATKPEMLPVAASSLRNDSSSSNRKAKNPDDGSSLHMAALPALFSLIIGAFGAL 235
 |||||
 Db 178 -----NEEALGFISSSLOGISIALTSLIIGFILGYI 212
 |||||
 QY 236 YKKRROP-SLTRAVENTIOIN--EEDNEISMLOEKEREFOEV 273
 |||||
 Db 213 YKKTKHPKSPESNETTQCHGCOEENEISMLOEKEREHLQV 253
 |||||

RESULT 13
 S29052

stem cell factor - human (fragments)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S29052
 R:Lu, H.S.; Clagston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderak, K.; Baltera
 ; Langley, K.E.
 Arch. Biochem. Biophys. 298, 150-158, 1992
 A:Title: Post-translational processing of membrane-associated recombinant human stem cell
 A:Reference number: S29052; MUID:92398336
 A:Accession: S29052
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUIH>
 C:Superfamily: mouse mast cell growth factor

Query Match 41.3%; Score 576.5; DB 2; Length 124;
 Best Local Similarity 75.2%; Pred. No. 1.3e-38;
 Matches 124; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

OY 26 EGTGRNRYNNVKDVTKLAVNLPKDYMITLKYPGMDVLPSCWISPMVQVLSLTDLL 85
 |||||
 DB 1 EGTGRNRYNNVK-----DVLPSHCWISPMVQVLS----- 30

OY 86 DKFSNISSEGLSNYSIIDKLAVNIDVLCVCKENSSKDLKSKSPEDRLFTPEEFERIFN 145
 |||||
 DB 31 DKFSNISSEGLSNYSII-----DVLVECVCKENSSKDLKSKSPEDRLFTPEEFERIFN 83

OY 146 RSIADFVYVASTSCCVVSSSTLSPEKDSRVSTKPFMLPPVAA 190
 |||||
 DB 84 RSI---DEVVASETSDCVVSSSTLSPEKDSRVSTKPFMLPPVAA 124

RESULT 14

B35971
 mast cell growth factor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35971
 R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
 Cell 63, 167-174, 1990
 A:Title: Identification of a ligand for the c-kit proto-oncogene.
 A:Reference number: A35971; MUID:91004215
 A:Accession: B35971
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-51 <WII>
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: transmembrane protein

Query Match 12.6%; Score 175.5; DB 2; Length 51;
 Best Local Similarity 72.3%; Pred. No. 1.8e-07;
 Matches 34; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 28 ICRNRVTNNVKDVTKLAVNLPKDYMITLKYPGMDVLPSCWISPMVQ 74
 |||||
 DB 3 ICGNPVTNDVKDITKLAVNLPNDYMITLNYVAGMDVLPSS-WIIDDMI 48

RESULT 15

A35971
 mast cell growth factor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: A35971
 R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
 Cell 63, 167-174, 1990
 A:Title: Identification of a ligand for the c-kit proto-oncogene.
 A:Reference number: A35971; MUID:91004215
 A:Accession: A35971
 A:Status: preliminary
 A:Molecule type: protein

A:Residues: 1-49 <WII>
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: transmembrane protein

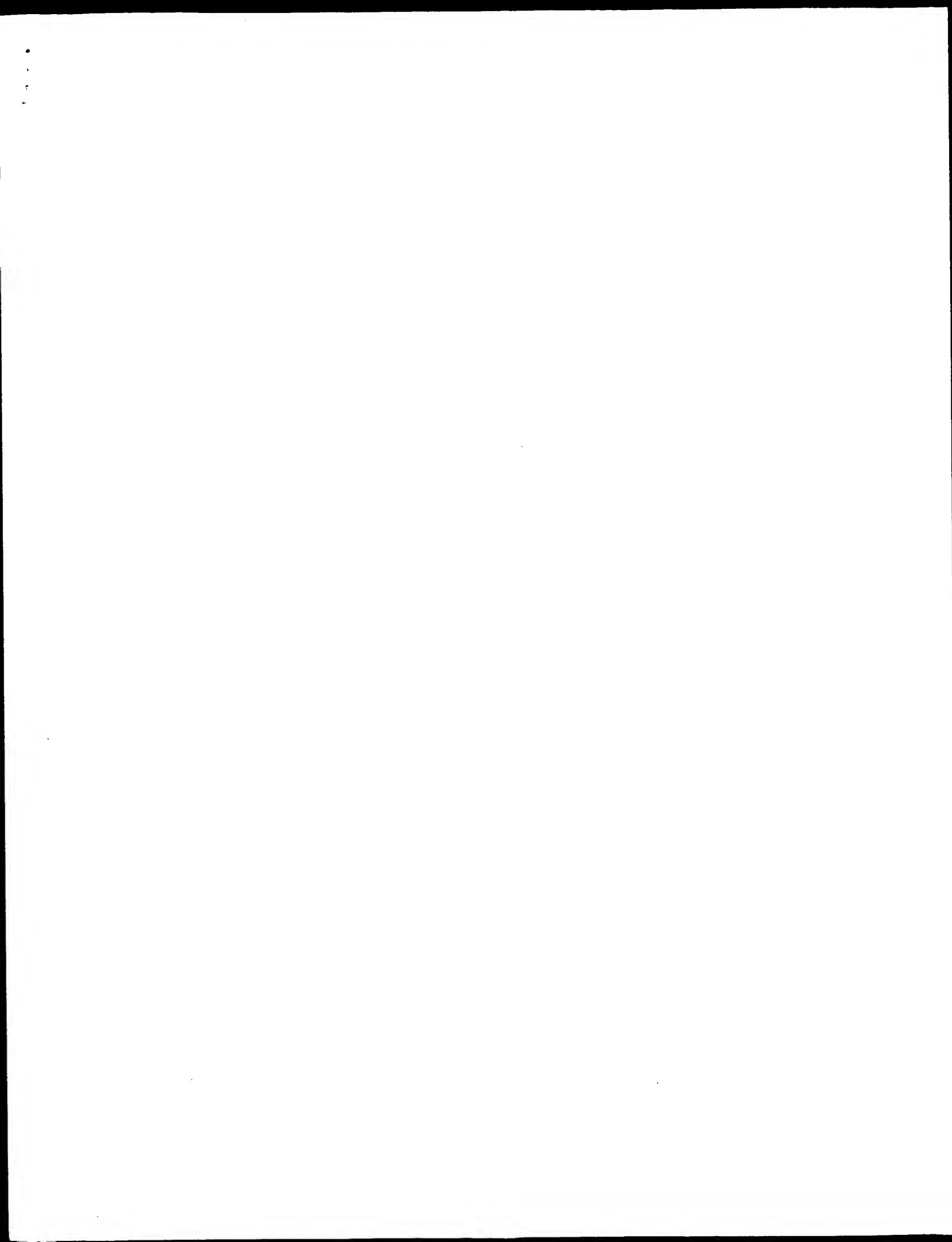
Query Match 12.3%; Score 172.5; DB 2; Length 49;
 Best Local Similarity 73.5%; Pred. No. 3e-07;
 Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;

OY 28 ICRNRVTNNVKDVTKLAVNLPKDYMITLKYPGMDVLPSCWISPMVQ 76
 |||||
 DB 3 ICGNPVTNDVKDITKLAVNLPNDYMITLNYVAGMDVLPSS-WY-DWVIG 48

Search completed: August 18, 2002, 13:03:15
 Job time: 120 sec

Sun Aug 18 14:09:04 2002

us-09-604-325a-61.rpt



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:02:05 ; Search time 35.93 Seconds

(without alignments)
294.195 Million cell updates/sec

Title: US-09-604-325A-61
Perfect score: 1397
Sequence: 1 MKKTQWILTCIVLQLLFN.....NEEDNELSMQEKREKREGEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	1 SCF_HUMAN	P21583 homo sapien
2	1203.5	86.1	274	1 SCF_PIG	Q20300 sus scrofa
3	1180.5	84.5	274	1 SCF_CANFA	Q06220 canis fam11
4	1157	82.8	273	1 SCF_MOUSE	P20826 mus musculu
5	857	61.3	201	1 SCF_RAT	P21581 rattus norv
6	703	50.3	287	1 SCF_CHICK	Q09108 gallus gall
7	107.5	7.7	989	1 PTP3_DICDI	P54637 dictyosteli
8	97.5	7.0	403	1 RAGE_MOUSE	Q6151 mus musculu
9	97	6.9	981	1 SCF4_RICE	Q9637 rickettsia
10	96.5	6.9	1742	1 MFSQ_HUMAN	Q9637 rickettsia
11	90	6.4	378	1 FDHA_METJA	Q9637 rickettsia
12	89.5	6.4	370	1 NRFE_HAETIN	Q9637 rickettsia
13	89	6.4	292	1 Y218_RICPR	Q9637 rickettsia
14	89	6.4	998	1 SCF4_RICAK	Q9637 rickettsia
15	88.5	6.3	1325	1 VAE6_SCHPO	Q09847 schizosacch
16	88.5	6.3	1815	1 UN13_CAEEL	P27713 caenorhabdi
17	88.5	6.3	1875	1 MLPI_YEAST	Q02455 saccharomyc
18	88	6.3	449	1 Y865_METJA	Q58275 methanococc
19	88	6.3	782	1 YAKB_SCHPO	Q09922 schizosacch
20	87.5	6.3	966	1 CAPP_MEDSA	Q02733 mediagao sa
21	87	6.2	402	1 RAGE_RAT	Q63495 rattus norv
22	87	6.2	469	1 C39A_HUMAN	Q9637 rickettsia
23	87	6.2	664	1 2AA4_CAEEL	Q09847 schizosacch
24	87	6.2	844	1 BR01_YEAST	Q09847 schizosacch
25	87	6.2	1202	1 Y801_SCHPO	P48582 saccharomyc
26	86.5	6.2	410	1 ARCA_BORBU	Q13798 schizosacch
27	86.5	6.2	451	1 DNAA_PASMU	Q51781 borrelia bu
28	86.5	6.2	466	1 DNAA_PROMI	Q9637 rickettsia
29	86.5	6.2	545	1 VNCS_JCQNV	P22837 proteus mir
30	86.5	6.2	729	1 CUL6_CAEEL	Q09054 junonia coe
31	86.5	6.2	1675	1 POL_RTBPV	Q21346 caenorhabdi
32	86.5	6.2	2492	1 TALA_DICDI	P27502 rice tungro
33	86	6.2	399	1 PX8D_HUMAN	P54633 dictyosteli

34	86	6.2	991	1 SCA4_RICAN	Q9a64 rickettsia
35	86	6.2	1146	1 KMAA_DICDI	P42527 dictyosteli
36	86	6.2	2238	1 ERPL_BUNYW	P20470 bunyomera
37	85.5	6.1	344	1 EMPA_YEAST	Q12480 saccharomyc
38	85.5	6.1	763	1 YN51_YEAST	P42843 saccharomyc
39	85	6.1	482	1 T2EA_YEAST	P36100 saccharomyc
40	85	6.1	618	1 YMX3_CAEEL	P34511 caenorhabdi
41	85	6.1	793	1 GAC1_YEAST	P28006 saccharomyc
42	85	6.1	935	1 COFG_YEAST	P32074 saccharomyc
43	84.5	6.0	520	1 APN2_YEAST	P38207 saccharomyc
44	84.5	6.0	665	1 YL14_CAEEL	Q11100 caenorhabdi
45	84.5	6.0	925	1 PDC2_YEAST	P32896 saccharomyc

ALIGNMENTS

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RESULT 1
ID SCF_HUMAN STANDARD: PRT: 273 AA.
AC P21583:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9104219; PubMed=2208279;
RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
RA Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
RA Fisher E.F., Ertayev H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs."
RL Cell 63:203-211(1990).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
CC PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
DR EMBL: M59964; AAA85450.1; -
DR PIR: A35974; A35974.
DR MIM: 184745; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT CHAIN 1 25
FT DOMAIN 26 273 KIT LIGAND.
FT TRANSMEM 26 214 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 215 237 POTENTIAL.
FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.

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FT DISULFID 68 163 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;

Query Match 100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-101;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYQLLFFNPLVKTBEICRRNRYNNKYDKYKLVANLPKRYMTTLKYPG 60
DB 1 MKKTQWITTCIYQLLFFNPLVKTBEICRRNRYNNKYDKYKLVANLPKRYMTTLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEVKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPPVAAASSLRNDSSSNRKAKNPPGSSLSHMAAALPALPSLIIGFAFGALYWK 240
DB 181 KPFMLPPVAAASSLRNDSSSNRKAKNPPGSSLSHMAAALPALPSLIIGFAFGALYWK 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273

RESULT 2
SCF_PIG 2
ID SCF_PIG STANDARD: PRT: 274 AA.
AC 029030:
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG OR MGF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=94146218; PubMed=7508758;
RA Zhang Z., Anthony R.V.;
RT "Porcine stem cell factor/c-kit ligand: its molecular cloning and
localization within the uterus.";
RT Biol. Reprod. 50:95-102(1994).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
PROBABLY INTERLEUKINS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
SECRETED SOLUBLE FORM.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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CC EMBL: L0786; AAA53670.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 274 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DISULFID 29 114 BY SIMILARITY.
FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 68 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 274 AA; 31118 MW; F93C8711AD7BA6A6 CRC64;

Query Match 86.1%; Score 1203.5; DB 1; Length 274;
Best Local Similarity 85.8%; Pred. No. 2.7e-86;
Matches 235; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKKTQWITTCIYQLLFFNPLVKTBEICRRNRYNNKYDKYKLVANLPKRYMTTLKYPG 60
DB 1 MKKTQWITTCIYQLLFFNPLVKTBEICRRNRYNNKYDKYKLVANLPKRYMTTLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEVKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVVSTLSPEKDSRVSVT 179
DB 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVVSTLSPEKDSRVSVT 180
QY 180 TKPFMLPPVAAASSLRNDSSSNRKAKNPPGSSLSHMAAALPALPSLIIGFAFGALYWK 239
DB 180 TKPFMLPPVAAASSLRNDSSSNRKAKNPPGSSLSHMAAALPALPSLIIGFAFGALYWK 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
DB 240 ROPSLTRAVENTIOINEDNEISMLOEKEREPOEV 274

RESULT 3
SCF_CANFA 3
ID SCF_CANFA STANDARD: PRT: 274 AA.
AC 006220:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG OR MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93106145; PubMed=1281786;
RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
Martin F.H.;
RT "Canine stem cell factor (c-kit ligand) supports the survival of
hematopoietic progenitors in long-term canine marrow culture.";
RT Exp. Hematol. 20:1118-1124(1992).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).

```

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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 CC -----
 DR EMBL: S53329; AAB24619.1; -
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 274
 FT TRANSMEM 26 215
 FT DOMAIN 216 238
 FT DISULFID 239 274
 FT DISULFID 29 114
 FT CARBOHYD 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT SEQUENCE 274 AA; 30869 MW; 4182BBAEDD0793B CRC64;
 Query Match 84.5%; Score 1180.5; DB 1; Length 274;
 Best Local Similarity 85.4%; Pred. No. 1.6e-84;
 Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MKKTQWILLCYLOLLEPLKTBICNRRTNNKDYTKLVANLPKDYMTLTKYVPG 60
 DB 1 MKKTQWILLCYLOLLEPLKTBICNRRTNNKDYTKLVANLPKDYMTLTKYVPG 60
 QY 61 MDVLPSCWISWVYVDSLDLDFKSNISGLSNYSIIDLVNIVDDLYECVENSS 120
 DB 61 MDVLPSCWISWVYVDSLDLDFKSNISGLSNYSIIDLVNIVDDLYECVENSS 120
 QY 121 KDIAKSKSEPPFLTPPEEFRRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKDSRVSV 179
 DB 121 ENVKAKPKSEPLRFLTPPEEFRRIFNRSIDAFKDFVAVSKSECVVSTLSPDKDSRVSV 180
 QY 180 TKPFMLPPVAASSLRNDSSSNKRAKPPGDSLSHMAALPALFSLIIGFAFALYMKK 239
 DB 181 TKPFMLPPVAASSLRNDSSSNKRAKSNISGDSMLQMAAALPALFSLVIGFAFALYMKK 240
 QY 240 RQPSLTRAVENTIQINEDNEISMLOEKEREFEV 273
 DB 241 KQPNLTRVETNIQINEDNEISMLOEKEREFEV 274
 RESULT 4
 SCF_MOUSE STANDARD: PRT; 273 AA.
 ID SCF_MOUSE
 AC P20826;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-MAY-1991 (rel. 18, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Klt growth factor (C-Klt ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF) (Hematopoietic growth factor Kt) (KL-1
 DE protein) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-WCB6F1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wigdall J.M., Eisenman J.,
 RA Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
 RA Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that
 RT is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 RT of the Klt-1 ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [13]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-WCB6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by
 RT alternative splicing and is missing in the Sld mutant.";
 RL Cell 64:1025-1035(1991).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.T., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
 RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
 RA Copeland N.G.;
 RT "Developmental abnormalities in Steel17H mice result from a splicing
 RT defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for steel regulation suggested by genomic and
 RT sequence analysis of the murine steel gene.";
 RL Genetics 142:927-934(1996).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=(102/ELIX3H/EL)F1; TISSUE=Brain;
 RA Gray J.;
 RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [17]
 RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 RT the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233(1990).
 RN [18]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murodock D.C.,
 RA Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,
 RA Galli S.J., Suggs S.V.;
 RT "Stem cell factor is encoded at the Sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [19]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [10]
 RP PARTIAL SEQUENCE OF 26-78.

RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene";
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY
 CC THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN
 CC VARYING RATIOS IN DIFFERENT TISSUES.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PIM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE
 CC ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR
 CC DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M59915; AAA40095.1; -;
 CC DR EMBL: M57647; AAA39538.1; -;
 CC DR EMBL: X68889; CAA48778.1; -;
 CC DR EMBL: U44724; -; NOT_ANNOTATED_CDS.
 CC DR EMBL: U44725; AAC52447.1; -;
 CC DR EMBL: X95381; CAA64667.1; -;
 CC DR EMBL: S40364; AAB22554.2; -;
 CC DR EMBL: M59912; AAA39539.1; -;
 CC DR PIR: A35971; A35971.
 CC DR PIR: A35972; A35972.
 CC DR PIR: A35975; A35975.
 CC DR PIR: A35976; A35976.
 CC DR PIR: A35977; A35977.
 CC DR PIR: A43751; A43751.
 CC DR PIR: B35971; B35971.
 CC MGD: MGI:96974; Kiti.
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF; 1.
 CC KW Growth factor; Glycoprotein; Transmembrane; Signal;
 CC Alternative splicing; Cell adhesion.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 273 KIT LIGAND.
 CC FT DOMAIN 26 214 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 215 237 POTENTIAL.
 CC FT DOMAIN 238 237 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 29 114 BY SIMILARITY.
 CC FT CARBOHYD 68 163 BY SIMILARITY.
 CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARAPPLIC 175 202 MISSING (IN SOLUBLE ISOFORM).
 CC FT VARIANT 207 215 A -> S.
 CC FT CONFLICT 215 215 W -> L (IN REF. 2).
 CC SEQUENCE 273 AA; 30645 MW; A7FC89B592A7967 CMC64;

Query Match 82.8%; Score 1157; DB 1; Length 273;
 Best local Similarity 82.8%; Pred. No. 1.1e-82;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
 1 MKKTQWITTCIYIOLLFLNPLVKTEIGICRNRYNNVADVTALVANKRDIWITIKYPPG 60

DB 1 MKKTQWITTCIYIOLLFLNPLVKTEIGICRNRYNNVADVTALVANKRDIWITIKYPPG 60
 QY 61 MDVLPSCHEISEMYYVOLDSLTLDLDRKSNISEGSLNIIIDKLVNIYDDLYECKEMSS 120
 DB 61 MDVLPSCHEISEMYYVOLDSLTLDLDRKSNISEGSLNIIIDKLVNIYDDLYECKEMSS 120
 QY 121 KOLKSKFSPEDRLPPEEFEPFNRSIDAFKDFVASTSPDCAVSTLSPKDSRSVST 180
 DB 121 KNKESPKRPERSPFPEEFEPFNRSIDAFKDFVASTSPDCAVSTLSPKDSRSVST 180
 QY 181 KPFMLPPVAASSLRNDSSSNRRKANPDGSSLHMAAALPALFSLIIGAFAGALYMKR 240
 DB 181 KPFMLPPVAASSLRNDSSSNRRKANPDGSSLHMAAALPALFSLIIGAFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEDNISMLOEKEREFOEV 273
 DB 241 QPSLTRAVENTIQINEDNISMLOEKEREFOEV 273
 RESULT 5
 SCF_RAT STANDARD; PRT; 201 AA.
 ID SCF_RAT
 AC P21581;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (mast
 DE cell growth factor) (Mgf) (Fragment).
 GN KITLG OR MGFF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91004219; PubMed=2208279;
 RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Tung J., Okino K.H.,
 RA Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
 RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
 RA Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J.C., Sachdev R.K.,
 RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
 RT "Primary structure and functional expression of rat and human stem
 RT cell factor DNAs";
 RL Cell 63:203-211(1990).
 RN [2]
 RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC STRAIN=BUFFALO; TISSUE=Liver;
 RX MEDLINE=91217037; PubMed=1708771;
 RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
 RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
 RT "Amino acid sequence and post-translational modification of stem cell
 RT factor isolated from buffalo rat liver cell-conditioned medium";
 RL J Biol. Chem. 266:8102-8107(1991).
 RN [3]
 RP SEQUENCE OF 26-39.
 RX MEDLINE=91004218; PubMed=2208278;
 RA Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
 RA Karake S.B., Sachdev R.K., Yuschenko V.N., Birkett N.C.,
 RA Williams L.R., Satyagal V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
 RA Langley K.E.;
 RT "Identification, purification, and biological characterization of
 RT hematopoietic stem cell factor from buffalo rat liver-conditioned
 RT medium";
 RL Cell 63:195-201(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.

CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -----
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 CC -----
 CC EMBL: M59966; AAA42117.1; -.
 CC PIR: B35974; B35974.
 CC PIR: A35973; A35973.
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF. 1.
 CC Growth factor: Glycoprotein; Transmembrane; Signal; Cell adhesion.
 CC SIGNAL 1 25
 CC CHAIN 26 >201
 CC MOD_RES 26 26 KIT LIGAND.
 CC DISULFID 29 114 PYRROLIDONE CARBOXYLIC ACID.
 CC CARBOHYD 68 163
 CC CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PARTIAL).
 CC CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
 CC CARBOHYD 167 167 O-LINKED (PROBABLE).
 CC CARBOHYD 168 168 O-LINKED (PROBABLE).
 CC CARBOHYD 180 180 O-LINKED (PROBABLE).
 CC CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (PARTIAL).
 CC NON_TER 201
 CC SEQUENCE 201 AA; 22537 MW; 1888686CDAF271B CRC64;
 SQ
 Query Match 61.3%; Score 857; DB 1; Length 201;
 Best Local Similarity 82.6%; Pred. No. 1.2e-59;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCIYQILLFNPVKTGICRNRVTNNKVDKLVANIPKRYMTTKVYVG 60
 DB 1 MKKTQWILTCIYQILLFNPVKTGICRNRVTNNKVDKLVANIPKRYMTTKVYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSISGLSNYSIIDKLVNIYVDLVCEVKESS 120
 DB 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSISGLSNYSIIDKLVNIYVDLVCEVKESS 120
 QY 121 KDLKSKSEPPRLTPEEFRRIFNRSIDAFKPVVASETSDCVSVSTLSPKEDSRVSVT 180
 DB 121 KDLKSKSEPPRLTPEEFRRIFNRSIDAFKPVVASETSDCVSVSTLSPKEDSRVSVT 180
 QY 121 KVKESLAKKETKFTPEEFSSIFNRSIDAFKDFVAVSDTSDCVSLSTLGPEDSRVSVT 180
 DB 121 KVKESLAKKETKFTPEEFSSIFNRSIDAFKDFVAVSDTSDCVSLSTLGPEDSRVSVT 180
 QY 181 KPFMLPPVAASSLRDSSSSN 201
 DB 181 KPFMLPPVAASSLRDSSSSN 201
 RESULT 6
 SCF_CHICK STANDARD; PRT; 287 AA.
 ID SCF_CHICK
 AC 009108;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF).
 GN KITLG.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN 11
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9373244; PubMed=7684722;
 RX Zhou J., Ohlaki M., Sakurai M.;
 RT "Sequence of a cDNA encoding chicken stem cell factor.";
 RL Gene 127:269-270(1993).

CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC EMBL: D13516; BAA02733.1; -.
 CC PIR: JN0637; JN0637.
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF. 1.
 CC Growth factor: Glycoprotein; Transmembrane; Signal; Cell adhesion.
 CC SIGNAL 1 25
 CC CHAIN 26 287
 CC MOD_RES 26 225
 CC DISULFID 247 287
 CC CARBOHYD 29 117
 CC CARBOHYD 68 167
 CC CARBOHYD 100 100
 CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 287 AA; 32328 MW; 6AE8556ADCL152578 CRC64;
 SQ
 Query Match 50.3%; Score 703; DB 1; Length 287;
 Best Local Similarity 51.9%; Pred. No. 1.6e-47;
 Matches 149; Conservative 50; Mismatches 74; Indels 14; Gaps 6;
 QY 1 MKKTQWILTCIYQILLFNPVKTGICRNRVTNNKVDKLVANIPKRYMTTKVYVG 60
 DB 1 MKKTQWILTCIYQILLFNPVKTGICRNRVTNNKVDKLVANIPKRYMTTKVYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLVNIYVDLVCEVKE 117
 DB 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLVNIYVDLVCEVKE 117
 QY 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLVNIYVDLVCEVKE 117
 DB 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLVNIYVDLVCEVKE 117
 QY 118 NSSKD-LKSKSEPPRLTPEEFRRIFNRSIDAFKPVVASETSDCVSVSTLSPKEDSRVSVT 175
 DB 121 DKNKDFIKENGLHYEDDFIPENFRIFNRSIDAFKPVVASETSDCVSVSTLSPKEDSRVSVT 180
 QY 176 RVSATKPPMLPPVAASSLRD-----SSSSNRKAKNPDDGSSLHMAALPALFSLIIG 229
 DB 181 RVAATKTPISPPVAASSLRDSSISGNTSSNKGKALGFISSISQIGISTALTSLSLIG 240
 QY 230 FAFGALYKRRKP-SLRVAVENIOIN--EEDNEISMIOEKEREQEV 273
 DB 241 FILGAIYKTKHKPSRPSNETIQCHGQENETISMIOEKEREHLQV 287
 RESULT 7
 PTP3_DICDI STANDARD; PRT; 989 AA.
 ID PTP3_DICDI
 AC P54637;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-
 DE phosphate phosphohydrolase 3).
 GN (PTP3 OR PTP3) AND (PTP2 OR PTP3).
 OS Dictyostelium discoideum (Slime mold).

Query Match 7.0%; Score 97.5; DB 1; Length 403;
 Best Local Similarity 26.2%; Pred. No. 1.9;
 Matches 42; Conservative 22; Mismatches 59; Indels 37; Gaps 7;

112 VECKENSSDLDKSKFSPPEPRFTPEEFRRINRSIDAKDFVASE-TSDCVASSTLS 170
 DB VHWIKDGLPLP-----APSPVLLPEVGH-----ADEGTYSCVATHPSH 307

171 PEKDSRYVTKPMPPLPVAASSLRNDSSSNRKAKNPQDSSILHMAALPAFSL-IIG 229
 DB GPQES-----PPV-----STRVETGDEGPAESGVSGSIGTIALALGILGLGVA 354

230 FARGALYKRRKP--SITRAVENIQTINEDNETISMLOEKE 267
 DB 355 LTVGAILMRKQPRRERKAPESQDEEERALEINQSEAE 394

RESULT 9
 SCA4_RICPE STANDARD; PRT; 981 AA.

AC 09AU37;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
 DE (Protein PS 120) (Fragment).
 GN SCA4 OR D.
 OS Rickettsia felis (Rickettsia azadi).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
 OX NCBI_TaxID=42862;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sekeyova Z., Roux V., Raoult D.;
 RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
 RT gene D coding for an intracytoplasmic protein.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -----
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 CC -----
 DR EMBL: AF196973; AAK31304.1; -
 KM Antigen.
 FT NON_TER 1 1
 FT NON_TER 981 981
 SO SEQUENCE 981 AA; 107514 MW; 7F1BF421E2C262E1 CRC64;

Query Match 6.9%; Score 97; DB 1; Length 981;
 Best Local Similarity 23.8%; Pred. No. 6.4;
 Matches 61; Conservative 33; Mismatches 84; Indels 78; Gaps 14;

19 FNPVLTGTCICRNRYTNVND-----VTKLVANLPKDYMITLKYPGM-DV 63
 DB 628 FNTAKTEAI--QWTTTQVLDSPIKAETKGTLESITKVAESPILNGQDKADYKMGGEA 685

64 LPSH-----CWISMVVQSLDSDLDDK-----FSNISEGLSNYSI----- 100
 DB 686 IASHTMAPTEKISTIESEVEGVASISTIDEDKRLMTKGLVEGITYEGRKANPEITSEKTKA 745

101 ----IDKLVNIVD--LVECVKE-----NSSKDLK-SFKSPPRLEFTPEEFRIIF 144
 DB 746 VSRGIDKSTALPDEKQALKDANEAALDRQNLTLEGAKRNLGEPFR-----DDIYNKA 801

145 NRSIDAFDFV-----ASETSDCVASSTLSPEKD-SNVSYTK-----PFMLPP 187

DB 802 QDVADALKNVITPVDAHPEKREVESEEE-VYKTTSSILINDISKLAIEKVNFRAMSPD 860
 QY 188 VAASSLRNDSSSNRK 203
 DB 861 GNLKTLKEKKAESTKK 876

RESULT 10
 MYSC_HUMAN STANDARD; PRT; 1742 AA.

AC 09NOX4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin Vc (Myosin 5C).
 GN MYOS5C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodriguez O.C., Cheney R.E.;
 RT "Cloning and characterization of myosin Vc, a third member of the
 RT myosin V family in vertebrates.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -I- SIMILARITY: CONTAINS 6 IQ DOMAINS.
 CC -I- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF272390; AAF78783.1; -
 DR InterPro: IPR002710; DIL.
 DR InterPro: IPR000048; IQ.
 DR Pfam: PF01843; DIL; 1.
 DR Pfam: PF00063; myosin_head; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR ProDom: PD003376; DIL; 1.
 DR SMART: SM00015; IQ; 5.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 4.
 KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KM Coiled coil; Polymorphism.
 FT DOMAIN 1 755
 FT MYOSIN HEAD-LIKE.
 FT 756 779
 FT DOMAIN 780 806
 FT 807 829
 FT DOMAIN 830 854
 FT 855 884
 FT DOMAIN 884 1351
 FT 1351 1574
 FT DOMAIN 1574 1679
 FT 1679 1742
 FT COILED COIL (POTENTIAL).
 FT P -> L.
 FT L -> S.
 FT VARIANT 634 634
 FT /FTID=VAR_010646.
 FT /FTID=VAR_010647.
 SO SEQUENCE 1742 AA; 202793 MW; 25DD3082A7B5AAB CRC64;

Query Match 6.9%; Score 96.5; DB 1; Length 1742;
 Best Local Similarity 21.4%; Pred. No. 15;
 Matches 60; Conservative 47; Mismatches 102; Indels 71; Gaps 14;

38 KDVTQVIANLPKDYM--ITLKVPQMDVLPKSHCHTSEKVVQVLSLND--LLDKFSN-- 90

Db 1369 EDEAKLIQNLIDLRKGVVNMIPG---LPAH--ILEWCYRYADSLDANMLKSLMNST 1423
 QY 91 -----ISEGLSNYSIIDKLVNIYDVLVECEYKENSNDKDKSKSPERL-----FTPE 138
 Db 1424 INCIKQVAVHEHLEDFEMLFSLNCHPLNCLIKQYSGEEFPMKHSPOONKNCJLNFDS 1483
 QY 139 EFERIFNR-SIDAFKDFVAVSET--DCVYSTLSPKDSRVSVTKPEMLPVAASSLRN 195
 Db 1484 EYKQILSDVAIRIYHOIITIMEKNIOPITVPGMLEYESLQGISGLK-----TGERK 1535
 QY 196 DSSSN-----RKANPPGDSLSLMAAALPALFSLITIGFARF 233
 Db 1536 RSSSIDFDGYMTSVLQOLSTFYTTMCNGIDP-----ELVROAVKOLFLLIGAVTLN 1589
 QY 234 ALYKKRQPSLTRAVENTIOINEEDNEISMLQE--KEREFQ 271
 Db 1590 SFLRKDMCKCRKMGQ-IRCN-----ISYLEMLKDKNKQ 1623

RESULT 11
 FDHA.METUA STANDARD; PRT; 378 AA.
 ID 060314:
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative formate dehydrogenase alpha chain (EC 1.2.1.2).
 GN M20006.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 ON NCBI_TaxID=2190;
 RX [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Utermack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RT Science 273:1058-1073(1996).
 RL MEDLINE=96337999; PubMed=8688087;
 CC -1- CATALYTIC ACTIVITY: Formate + NAD(+) = CO(2) + NADH.
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN), ZINC, FAD, MAY BIND 4 FE-4S
 CC CLUSTER (BY SIMILARITY).
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY.
 CC
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 CC
 CC EMBL: U67459; AAB97987.1; -
 CC HSSP: P07658; IAA6.
 DR TTR; MU0006;
 DR InterPro: IPR001467; Molybdopterin.
 DR Pfam: PF00384; molybdopterin; 2.
 DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
 DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
 DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; FALSE NEG.
 KM Hypothetical protein; Oxidoreductase; Zinc; Flavo-protein; Molybdenum;
 KM FAD; NAD; Iron-sulfur; 4Fe-4S; Complete proteome.
 FT METAL 8 8 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

FT METAL 11 11 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 15 15 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 43 43 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SO SEQUENCE 378 AA; 42050 MW; EC013060FE2609AA CRC64;

Query Match 6.4%; Score 90; DB 1; Length 378;
 Best Local Similarity 21.3%; Pred. No. 6.7;
 Matches 66; Conservative 31; Mismatches 91; Indels 122; Gaps 16;

QY 12 IYIQLLEFNPVKTG-----ICRNRTNNKQVT-----K 42
 Db 53 IYHKKRLKPLIKKNGKLVETWDEALSFIAEKIKYNADITFIASGCKTNEQNALRK 112
 QY 43 LV-----ANLKK-----DYMITLKVPGM-----DVLPSCHWSEWVQLSDS 80
 Db 113 LVDSLAKIIGHICNSPRVYAEVSTTIDENAKNIIITIGDVFSEALIGKVIKAKK 172
 QY 81 LTDL-----LDKF-----SNISEGLSNYS-----IIDKLVINIYDVLVECKE 117
 Db 173 GSKYITFTEKEKELIKLNADFEVAVDSILGVDSLNVQKNTIIINAPVN-VDEIKTAKE 231
 QY 118 NSSKDL--KKSFKSPEPRL-----FTPEEFRTNRS-----IDAFK--DF 154
 Db 232 NKAIVLPVAKHNTVGAATLIGIPALNKDEYFELLKNSKFLYIMGENPALVDKDKVVEF 291
 QY 155 VV-----ASEISDCVYSTLSPKDSRVSVTKPEMLPVAASSLRNSSSN--RKAK 205
 Db 292 LVVODITMTETAKMDVVLPSICWAERD-----GTPIINTDKRIQIKAKV 336
 QY 206 NPPGDSLSLHW 215
 Db 337 NPPGDAMDMD 346

RESULT 12
 NRFF_HAEIN STANDARD; PRT; 370 AA.
 ID NRFF_HAEIN
 AC P44942;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c-type biogenesis protein nrff precursor.
 GN NRFF OR H10934.
 GN Cytochrome c-type biogenesis protein nrff precursor.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 ON NCBI_TaxID=727;
 RX [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
 RA Mckenney K., Sutton G., Fitzgerald W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utermack T.R., Hanna M.C., Nguyen D.T., Sauder D.W., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
 RA Ghem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RT Science 269:496-512(1995).
 RL science 269:496-512(1995).
 CC -1- FUNCTION: MAY BE REQUIRED FOR THE BIOGENESIS OF C-TYPE
 CC CYTOCHROMES. POSSIBLE SUBUNIT OF A HEME LYASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE CCMH/CYCL/CC12/NRFF FAMILY.
 CC
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DR EMBL: U37775; AAC22592.1; ALT_INIT.
DR TIGR: H10934;
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 1.
KW Cytochrome c-type biogenesis; Periplasmic; Heme; Signal;
KW Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 370 CYTOCHROME C-TYPE BIOGENESIS PROTEIN
FT BINDING 47 47 NRRF.
FT BINDING 50 50 HEME (COVALENT) (POTENTIAL).
FT BINDING 50 50 HEME (COVALENT) (POTENTIAL).
SQ SEQUENCE 370 AA; 42161 MW; 4023B680D7FA9A80 CRC64;

Query Match 6.4%; Score 89.5; DB 1; Length 370;
Best Local Similarity 25.6%; Pred. No. 7.1;
Matches 57; Conservative 25; Mismatches 82; Indels 59; Gaps 12;

QY 68 CWISEVYQVDSLTDL-LDKFENISEGLSNYSIIDKLVNIYDLYECVKNSSDKLKS 126
DB 50 CONQNLVESNSPIAYDLRLVKKVMDGKSNQOIIDKMTARQDFV-----NYKPP 100
QY 127 FK-----SPEPLTFPEEFERFIRNSIDAFKDFVASETSDCVSTLSPEKDSRY 178
DB 101 FKNMTALLMLPALLILAAVLLYFSNRK---KQF-----SEKVVQQL--ENDEITIS 148
QY 179 VYKPFLLPVYAASSLANDSSSKRAKKNPPGSSLLHMAALPALFSLITGAFGALYV- 237
DB 149 -----LPSTFGSSPPKQGEPS--KLSKGVNSKIYF-----VFETLLI--ALPATYTF 192
QY 238 -----KKRQPSLTRAVENTIOINE--DNEISMLOEKER 268
DB 193 SLDRFSRVOQGQSMIECHNQVEMNDKHNENVIKLIKONKLR 235

RESULT 13
Y218_RICPR STANDARD; PRT; 292 AA.
AC 005944;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glycosyl transferase Rp128 (EC 2.4.1.16).
GN RP218.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=782;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RA MEDLINE=97419517; PubMed=9274032;
RA Andersson J.O., Andersson S.G.E.,
RT "Genomic rearrangements during evolution of the obligate
intraacellular parasite Rickettsia prowazekii as inferred from an
analysis of 5205 bp nucleotide sequence.",
RL Microbiology 143:2783-2795(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Madrid E;
RA MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichenitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.",
RL Nature 396:133-140(1998).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. WAAE/KDTPX
CC SUBFAMILY.

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DR EMBL: Y11780; CAI72466.1;
DR InterPro: IPR001173; Glycosyltransf_2.
DR Pfam: PF00535; Glycosyltransf_2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 292 AA; 33902 MW; 45EF7570B05A270 CRC64;

Query Match 6.4%; Score 89; DB 1; Length 292;
Best Local Similarity 21.1%; Pred. No. 5.8;
Matches 68; Conservative 53; Mismatches 111; Indels 90; Gaps 16;

QY 1 MKKTQWLTGCIYQLLFNPLVTEGICRRVYNNKVDYK---LVANLPKDYMITLKY 57
DB 1 MKKISTFIIT-----KNESARIARAINVKNTIDEVIYVNDNESTDVTIAIK 47
QY 58 VPGMDVLPSCWISQM-VVQLSDSLTDLKFSNISEGLSNYSIIDKLVNIYDLYECVK 116
DB 48 TLGAQVIVKP-WLGVGQKSPAESMC-----VNWVNLINADDELSELODEIFYIF 98
QY 117 ENSKDLKKSPPK-----SPEPLTFP-EEFRFIRFNSIDAFKDFVASETSDCVS 166
DB 99 TSHNODRLAYQIKLLIMYRGDQPRMFAPLNLCTRLNKKFASFN-TINSTTHDSYVF 157
QY 167 STLSPEKDSRYSVT-KPEMLPVYA-----ASSLNDSSSSNRKAKNP 207
DB 158 N-----KD--VDFTGKIYLLNGIAIYHSGTSIBLVKNAFYSSQAKDLVYKQCKLSNP 210
QY 208 PGDSSLHMAALPALF-----SLITGAFGALYKKRQPSLTRAVENTIOI 253
DB 211 RLATEMTWC--FLKAFPIRRYFVGFDVDSIIIFAFARFLRLAKRLDLSL---KSNV 264
QY 254 NEEDNEI-----SMLOEKER 268
DB 265 ITSDNYITNYCMDFRSLQOKKR 286

RESULT 14
SCA4_RICAK STANDARD; PRT; 998 AA.
AC 09AIX9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (P6120) (120 kDa antigen)
DE (Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia akari.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=786;

RN [1]
RP SEQUENCE FROM N.A.
RA Sekeyova Z., Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing sequence of the
RT 'gene D' coding for an intracytoplasmic protein.",
RL Submit (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -----

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 CC -----
 CC EMBL: AF213016; AAK30691.1; .
 CC Antigen.
 CC KW Antigen.
 CC NON_TER 1 1
 CC FT 998 998
 CC SEQUENCE 998 AA; 109328 MW; FCEBA3AC62DE5BD5 CRC64;

Query Match 6.4%; Score 89; DB 1; Length 998;
 Best Local Similarity 22.5%; Pred. No. 27;
 Matches 58; Conservative 37; Mismatches 77; Indels 86; Gaps 13;

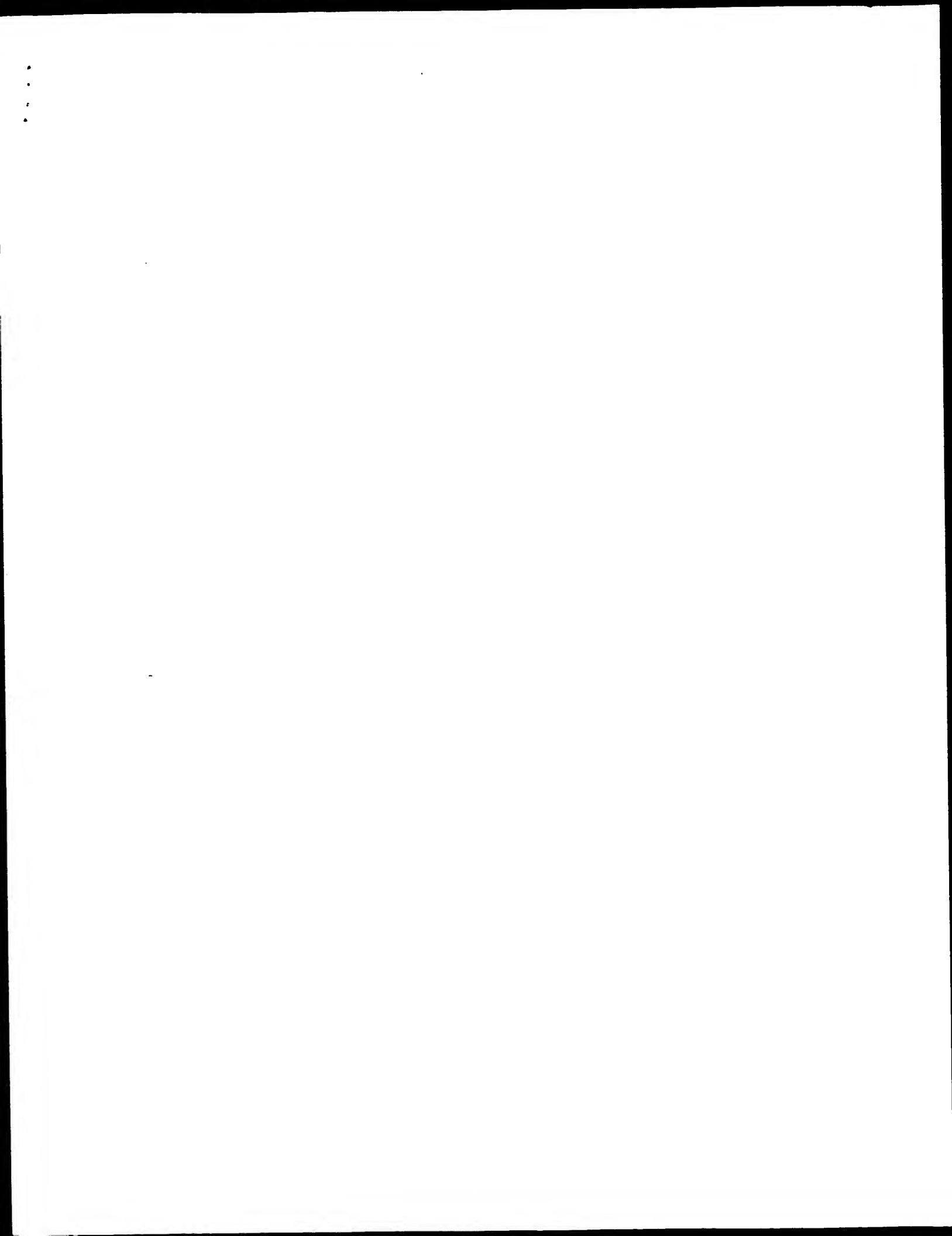
QY 19 FNLVTEGICRRNRYNNV-----VTKLVANLPKRYMTLKYVPGM-DV 63
 Db 636 FNTAKTAAL--OKVTKVLDSPTAEIKGETLSTIKTIVAESPLNVQKTDIVKGMGA 693
 QY 64 LPSH-----CWISENVVQLSDSLFDLDDK-----FSN 90
 Db 694 IASHRTWAPTKTIAIESVETGVAKSTTDLDEKRLMTKGLVDGIYEDKANPEITSEMMKA 753
 QY 91 ISEGLSNVSTIDKLVNVD-----LVECKENSSKDLK-KSPKSPPEPLRFPPEEFFRIE 144
 Db 754 VSKGVNSTAIPEDKQALKDAASEALDRATONFTBGLKQNLDEPKPR-----DDIY 806
 QY 145 NRSID--AFKDFVASETSDCVSSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSS-- 199
 Db 807 NKADIDVIALKN-----VTTVLDANPKEKREVSSEEVN--NKTSSILNDISKIA 853
 QY 200 ----SNRKANPEGSSSL 213
 Db 854 IEKYNLRLAMLSL-DSNL 870

RESULT 15
 YAE6_SCHPO
 ID YAE6_SCHPO STANDARD; PRT: 1325 AA.
 AC 009847;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Hypothetical 145.8 kDa protein C23D3.06C in chromosome I.
 GN SPAC23D3.06C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Nidlett D., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: Z64354; CAA91241.1; .
 CC KW Hypothetical protein.
 CC SEQUENCE 1325 AA; 145776 MW; EEPD952FB7F0E6BD CRC64;

Query Match 6.3%; Score 88.5; DB 1; Length 1325;
 Best Local Similarity 20.7%; Pred. No. 43;
 Matches 60; Conservative 38; Mismatches 91; Indels 101; Gaps 12;

QY 18 LFNPLVTEGICRRNRYNNV-----KDYTKLVANLPK-----DYMITLKYVPGMDV 63
 Db 717 IFGTAETQ--VECKRPENNVLTKRPFSPAPSDKSNFPAANIPSAGEGLDOCKTSTALP----- 771
 QY 64 LPSHCWISENVVQLSDSLFDLDDK-----SNISEG--LSNVSTIDKL 104
 Db 772 -----STGITKLSENDNEKAESNETKGQNTTIAKONKSSKSEKASVANMSALNKS 824
 QY 105 VNIVDDLVECKENSSKDLKSKSPPEPLRFPPEEFFRIINRSIDA-FKDFVVAASETSDC 163
 Db 825 TN-----NETSDSKPSLTKSP-----LEFSAADAPFTFNKPSSTPPF 861
 QY 164 VVSSSTLSPEKDSRVSVT-----KPFMLPPVAASSLRNDSSSSNRKAKNPPGSSLIHMAAM 218
 Db 862 SFNKP-L-VEKESKQDVSDTSRSPFSFKACIDSKKSPTEPPTMAESNTISESEGWKLI 920
 QY 219 ALPALFSLILGFARFALYKKRQPSLRPAVENIQINEEDNEISMLOKER 268
 Db 921 EQPNVES-----EIEDODESSDLNGKRR 944

Search completed: August 18, 2002, 13:02:07
 Job time: 52 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:06:04 ; Search time 114.11 Seconds
(without alignments) 413.878 Million cell updates/sec

Title: US-09-604-325a-61
Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEMISLQEKEREPQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTRMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rhizobium:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rv1virus:*
17: sp_bacteriophage:*
18: sp_archaeophage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	87.2	245	4	Q9UOK7
2	1217.5	87.2	274	6	P79169
3	1187.5	85.0	274	6	Q95M19
4	1184.5	84.8	274	6	Q28132
5	1180.5	84.5	274	6	Q95N18
6	1158	82.9	273	11	Q90W4
7	1157	82.8	273	11	Q921N5
8	1156.5	82.8	267	6	P79368
9	1154.5	82.6	261	6	Q95MD2
10	1150	82.3	273	11	Q62524
11	1149	82.2	276	6	P97332
12	1117.5	80.0	256	6	O62765
13	1000	71.6	245	11	Q922E7
14	991.5	71.0	260	6	Q95MNS
15	978	70.0	245	11	Q64222
16	865	61.9	208	11	Q64384

17	702	50.3	287	13	Q90314
18	589	42.2	253	13	Q90315
19	509	36.4	123	11	Q61854
20	401.5	28.7	96	6	Q95MG8
21	375	26.8	271	13	Q9YGP2
22	251	18.0	54	4	Q16487
23	223.5	16.0	47	6	Q95MG7
24	214.5	15.4	51	6	Q9N1Y5
25	136	9.7	36	6	Q9TU74
26	106	7.6	465	16	Q97H56
27	105.5	7.6	1498	3	Q9P884
28	105.5	7.6	1498	3	Q96VK6
29	102	7.3	792	5	Q9BP03
30	101	7.2	1490	5	Q19545
31	100.5	7.2	402	11	Q35444
32	100.5	7.2	647	16	Q98P9
33	100	7.2	1501	3	Q96VL9
34	99	7.1	937	10	Q9MAL4
35	97.5	7.0	1107	3	Q12271
36	97	6.9	1447	16	Q9PQJ8
37	97	6.9	1566	11	Q9R1L5
38	96.5	6.9	475	11	Q9D6C8
39	96	6.9	3072	12	Q92645
40	95.5	6.8	484	5	Q01626
41	95.5	6.8	614	5	Q9LQ29
42	95.5	6.8	683	2	Q50281
43	95.5	6.8	806	2	Q9L8P7
44	95.5	6.8	1515	3	Q96VK4
45	94.5	6.8	576	11	Q62970

ALIGNMENTS

RESULT 1
ID Q9UOK7 PRELIMINARY: PRT: 245 AA.
AC Q9UOK7;
DT 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160429; PubMed=10049787;
RA Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;
RT "Parathyroid hormone-regulated production of stem cell factor in human
RL Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF119835; AAD22048.1; -;
DR EMBL; AF400437; AAK92486.1; -;
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 245 AA; 27903 MW; FF87983163A3C36 CRC64;

Query Match 87.2%; Score 1218; DB 4; Length 245;
Best Local Similarity 88.3%; Pred. No. 1,6e-94;
Matches 241; Conservative 1; Mismatches 3; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVETGICRRNRYNNVKKDYTKLVANLPKRYMTLTKVYVG 60
DQ 1 MKKTQWILTCIYLQLLFNPLVETGICRRNRYNNVKKDYTKLVANLPKRYMTLTKVYVG 60
QY 61 MDVLPSCWISSEWVQVLSLTLDDKFSNISEGLSNYSIIDRLVNIYVDLVECVKENS 120

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Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVCEKVENSS 120
QY 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 180
Db 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 174
QY 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
Db 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 212
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245

RESULT 2
P79169
ID P79169 PRELIMINARY; PRT; 274 AA.
AC P79169;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE STEM CELL FACTOR.
GN SCF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97069946; PubMed=8912926;
RA Dunham S.P., Onions D.E.;
RT "The cloning and sequencing of cDNAs encoding two isoforms of feline
RT stem cell factor."
RL DNA Seq. 6:233-237(1996).
DR EMBL: D50833; BAA09445.1; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 274 AA; 30987 MW; C5B78DB4791237BE CRC64;

Query Match 87.2%; Score 1217.5; DB 6; Length 274;
Best Local Similarity 87.2%; Pred. No. 2e-94;
Matches 239; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQTWITTCIYQLDLEFNPLVKTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
Db 1 MKKTQTWITTCIYQLDLEFNPLVKTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVCEKVENSS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVCEKVENSS 120
QY 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 179
Db 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 179
QY 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 239
Db 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 KOPNLTRIVENQIINEDNEISMLOEKEREFOEV 274

RESULT 3
Q95M19 PRELIMINARY; PRT; 274 AA.
AC Q95M19;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE STEM CELL FACTOR.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SHIBA; TISSUE=BRAIN;
RA Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT "Identification of Splicing Isoforms of Caprine Stem Cell Factor
RT (SCF) Transcripts and Expression Patterns of the Two Major Isoforms,
RT gSCF825 and gSCF741, in the Brain and the Skin of Adult and Fetal
RT Shiba Goats, Capra hircus."
RL Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB002152; BAB71733.1; -
SQ SEQUENCE 274 AA; 31052 MW; BBFE69A509EF65D CRC64;

Query Match 85.0%; Score 1187.5; DB 6; Length 274;
Best Local Similarity 85.0%; Pred. No. 6.7e-92;
Matches 233; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKKTQTWITTCIYQLDLEFNPLVKTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
Db 1 MKKTQTWITTCIYQLDLEFNPLVKTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVCEKVENSS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVCEKVENSS 120
QY 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 179
Db 121 KDKKSKSPERPLFPPEEFRIINRSIDAFKDPVVASSTSDCVSSTLSPEDSRVSV 179
QY 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 239
Db 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 KOPNLTRIVENQIINEDNEISMLOEKEREFOEV 274

RESULT 4
Q28132 PRELIMINARY; PRT; 274 AA.
AC Q28132;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE STEM CELL FACTOR LONGER ISOFORM.
GN SCF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SPLEEN;
RA MEDLINE=94339176; PubMed=7520283;
RA Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
RT "Cloning and characterization of cDNAs encoding two normal isoforms of
RT bovine stem cell factor."
RL Biochim. Biophys. Acta 1223:148-150(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RA Kudo T.;
RT "Bovine counterpart of stem cell factor."
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; D28934; BAA06061.1; -.
 DR EMBL; AB033716; BAA94808.1; -.
 DR InterPro; IPR003453; SCF.
 DR Pfam; PF02404; SCF; 1
 SO SEQUENCE 274 AA; 31014 MW; D6C1DDB77B0CB12B CRC64;

Query Match 84.8%; Score 1184.5; DB 6; Length 274;
 Best Local Similarity 84.7%; Pred. No. 1.2e-91;
 Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 D 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 D 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEPEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRSV 179
 D 121 ENVAKSKSPERQFTEPEKFEIJKSIDAFKOLEIVASMSSECVISSTSPKDSRSV 180
 QY 180 TKPFMLPPVAASSLRNDSSSNRKAAPPDSSLIHMAALPALFLSLIIGFAFGALYWK 239
 D 181 TKPFMLPPVAASSLRNDSSSNRKAANSIDSSLOMAVALPAFFSLVIGFAFGALYWK 240
 QY 240 RPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 D 241 KQPLTRTVENRQINEDNEISMLOEKEREFOEV 274

RESULT 5
 ID 095N18 PRELIMINARY; PRT; 274 AA.
 AC 095N18;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE STEM CELL FACTOR LONG ISOFORM.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett R.D., Murphy B.D.;
 RT "Stem cell factor long form."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF013712; AAG37434.1; -.
 SO SEQUENCE 274 AA; 31034 MW; 5AC1619014AESE72 CRC64;

Query Match 84.5%; Score 1180.5; DB 6; Length 274;
 Best Local Similarity 84.3%; Pred. No. 2.6e-91;
 Matches 231; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 D 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 D 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEPEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRSV 179
 D 121 ENVAKSKSPERQFTEPEKFEIJKSIDAFKOLEIVASMSSECVISSTSPKDSRSV 180
 QY 180 TKPFMLPPVAASSLRNDSSSNRKAAPPDSSLIHMAALPALFLSLIIGFAFGALYWK 239
 D 181 TKPFMLPPVAASSLRNDSSSNRKAANPLGDSNLOMAVALPAFFSLVIGFAFGALYWK 240

QY 240 RPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 D 241 KQPLTRTVENRQINEDNEISMLOEKEREFOEV 274

RESULT 6
 ID 090W24 PRELIMINARY; PRT; 273 AA.
 AC 090W24;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DE STEM CELL FACTOR KL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Teramoto T., Nagashima M., Thorgerisson S.S.;
 RT "Rat-SCF-KL-1."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF071204; AAD02827.1; -.
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF; 1
 SO SEQUENCE 273 AA; 30712 MW; C0F56527DC93FD27 CRC64;

Query Match 82.9%; Score 1158; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 2e-89;
 Matches 225; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 D 1 MKKTQWILTCIYQLLFLNPLVTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 D 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVNVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEPEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRSV 180
 D 121 KVKESLAKPETRNFTEPEFSIFNRSIDAFKDFVAVADTSDCVLSTLSPKDSRSV 180
 QY 181 KPFMLPPVAASSLRNDSSSNRKAAPPDSSLIHMAALPALFLSLIIGFAFGALYWK 240
 D 181 KPFMLPPVAASSLRNDSSSNRKAASPEDEGLQWTAMALPALISLVIGFAFGALYKK 240
 QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 D 241 QSSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 7
 ID 092IN5 PRELIMINARY; PRT; 273 AA.
 AC 092IN5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE SIMILAR TO KIT LIGAND.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011322; AAH11322.1; -.
 SO SEQUENCE 273 AA; 30661 MW; A7FC91E339320107 CRC64;

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Query Match      82.8%; Score 1157; DB 11; Length 273;
Best Local Similarity 82.8%; Pred. No. 2.4e-89;
Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVPG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKKTQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVAG 60

QY 61 MDVPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MDVPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNAP 120

QY 121 KDKKSPKSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSVT 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KDKKSPKSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSVT 180

QY 181 KPFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KPFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 240

QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFORY 273
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QPSLTRAVENTIOINEDNEISMLOEKEREFORY 273

RESULT 8
P79368 PRELIMINARY; PRT: 267 AA.
ID P79368; Q28591;
AC 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
RT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE STEM CELL FACTOR (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE OF 8-267 FROM N.A.
RC TISSUE=OVARIAN FOLLICLE;
RA Tisdall D.J., Quirke L.D.;
RN Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE OF 1-202 FROM N.A.
RC TISSUE=OVARIAN FOLLICLE;
RA Tisdall D.J., Quirke L.D.;
RN Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE OF 1-202 FROM N.A.
RC TISSUE=OVARIAN FOLLICLE;
RA Tisdall D.J., Quirke L.D.;
RN Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U69874; AAB49491.1;
DR EMBL: Z50743; CAA90620.1;
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
FT NON_TER 267
SQ SEQUENCE 267 AA; 30148 MW; 9D9D959E4B9EC841 CRC64;

Query Match      82.8%; Score 1156.5; DB 6; Length 267;
Best Local Similarity 85.0%; Pred. No. 2.6e-89;
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKKTQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVPG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKKTQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVAG 60

QY 61 MDVPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 61 MDVPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KDKKSPKSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSVT 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ENKSKSPSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSV 180

QY 180 TKFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 TKFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 240

QY 240 RQPSLTRAVENTIOINEDNEISMLOEK 266
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 KQPSLTRAVENTIOINEDNEISMLOEK 267

RESULT 9
Q95MD2 PRELIMINARY; PRT: 261 AA.
ID Q95MD2;
AC Q95MD2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MAST CELL GROWTH FACTOR (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cochran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF401625; AAK94474.1;
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 261 AA; 29526 MW; 16A3062105346E4B CRC64;

Query Match      82.6%; Score 1154.5; DB 6; Length 261;
Best Local Similarity 86.6%; Pred. No. 3.7e-89;
Matches 226; Conservative 19; Mismatches 15; Indels 1; Gaps 1;

QY 4 TQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVGMV 63
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 TQWITTCIYIQLLEFNPVKTGICRNRYNNVKKVTKLVANLPKDYMITLKYVGMV 60

QY 64 LPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNSSKD 123
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LPSHCWISSEMYVQSDSLTDLDKFSNISSEGLSNTSIIDKLVNIYVDLVECKEKNSS 120

QY 124 KSKSPSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSVT 182
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KSKSPSEPEPLFTPEEFRIENRSIDAFKDFVAVASSTDCVVSSTLSPKDSRVSVT 180

QY 183 FMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 242
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYWKRR 240

QY 243 SLTRAVENTIOINEDNEISMLOEK 263
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SLTRAVENTIOINEDNEISMLOEK 261

RESULT 10
Q62524 PRELIMINARY; PRT: 273 AA.
ID Q62524;
AC Q62524;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MAST CELL GROWTH FACTOR.
GN KITL OR MGF.

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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBL_TaxID=10090;
 RP [1]
 RC STRAIN=C3H/EL; TISSUE=BRAIN;
 RX MEDLINE=97032534; PubMed=8875893;
 RA Graw J., Loester J., Neuhauser-Klaus A., Pretsch W., Schmitt-John T.,
 RT "Molecular analysis of two new Steel mutations in mice shows a
 transversion or an insertion."
 RL Mamm. Genome 7:843-846(1996).
 DR EMBL; X99322; CAA67698.1; -
 DR MGD; MGI:96974; KIL.
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF. 1.
 FT VARIANT 193 193
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30645 MW; B3E9D0B72C734107 CRC64;

Query Match 82.3%; Score 1150; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 9.4e-89;
 Matches 225; Conservative 19; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKKTQWITCTIYQLLFNPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWITCTIYQLLFNPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEVNVVSDSLTDLDFNSISGLSNYSITDKLVNIVDDLYECVENS 120
 DB 61 MDVLPSCWISSEVNVVSDSLTDLDFNSISGLSNYSITDKLVNIVDDLYECVENS 120
 QY 121 KDLKSKSPPEPLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 DB 121 KDLKSKSPPEPLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 QY 121 KNIKESKRPETRSFTPEEFISFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 DB 121 KNIKESKRPETRSFTPEEFISFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAALPALFSLITGFAFGALYWKRR 240
 DB 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAALPALFSLITGFAFGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 11
 P97332 PRELIMINARY; PRT; 273 AA.
 AC P97332;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF S1-3NEU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBL_TaxID=10090;
 RP [1]
 RC STRAIN=C3H/EL; TISSUE=BRAIN;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhauser-Klaus A., Pretsch W., Schmitt-John T.,
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
 gene defines a novel allele at the Steel locus with a weak
 phenotype."
 RL Mamm. Genome 7:843-846(1996).
 DR EMBL; Y10287; CAA71329.1; -
 DR MGD; MGI:96974; KIL.
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF. 1.
 FT VARIANT 193 193 P -> L.

FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

Query Match 82.2%; Score 1149; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 1.1e-88;
 Matches 225; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKTQWITCTIYQLLFNPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWITCTIYQLLFNPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEVNVVSDSLTDLDFNSISGLSNYSITDKLVNIVDDLYECVENS 120
 DB 61 MDVLPSCWISSEVNVVSDSLTDLDFNSISGLSNYSITDKLVNIVDDLYECVENS 120
 QY 121 KDLKSKSPPEPLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 DB 121 KDLKSKSPPEPLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 QY 121 KNIKESKRPETRSFTPEEFISFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 DB 121 KNIKESKRPETRSFTPEEFISFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYT 180
 QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAALPALFSLITGFAFGALYWKRR 240
 DB 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAALPALFSLITGFAFGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 12
 062765 PRELIMINARY; PRT; 256 AA.
 AC 062765;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
 GN EGF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN NCBL_TaxID=9796;
 RP [1]
 RC SEQUENCE FROM N.A.
 RA TISSUE=SKIN.
 RT Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.,
 RL "An equine sequence homologous to stem cell factor (KIT-ligand)."
 DR EMBL; AF053498; AAC97076.1; -
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF. 1.
 FT NON_TER 1 1
 FT NON_TER 256 256
 SQ SEQUENCE 256 AA; 28933 MW; 9E4876CAEC7B55FE CRC64;

Query Match 80.0%; Score 1117.5; DB 6; Length 256;
 Best Local Similarity 86.3%; Pred. No. 4.6e-86;
 Matches 221; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 12 IYIQLLFPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVGMDVLPSCWIS 71
 DB 1 IYIQLLFPVTEGICRRNRYNNKDVTKLVANLPKDYMITLKYVGMDVLPSCWIS 71
 QY 72 EMYVOLSITLTLDFKFSNISGLSNYSITDKLVNIVDDLYECVENSMDLKKRSPE 131
 DB 72 EMYVOLSITLTLDFKFSNISGLSNYSITDKLVNIVDDLYECVENSMDLKKRSPE 131
 QY 132 PRLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYTKPFLPVA 190
 DB 132 PRLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYTKPFLPVA 190
 QY 121 SRLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYTKPFLPVA 180
 DB 121 SRLTFPEEFRIKNSIDAFKDFVVASETSDCVSVSTLSPKDSRVSYTKPFLPVA 180
 QY 191 SSLRNDSSSNRKAKNPBGDSLHMAALPALFSLITGFAFGALYWKRRQPSLTRAVEN 250

D0	181	SSLRRDSSSSRRKRSNFTGDSNLOMAALPAFTSLVYGFAGALYKKRQPNLTRAVEN	240
QY	251	IQINEEDNEISMLOEK	266
D0	241	IQINEEDNEISMLOEK	256

RESULT	ID	PRELIMINARY:	PRT:
13	09Z2E7		245 AA.
AC	09Z2E7.		
DT	01-MAY-1999	(TREMBlrel. 10, Created)	
DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)	
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)	
DE	STEM CELL FACTOR KL-2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Teramoko T., Nagashima M., Thorgerlsson S.S.;		
RT	"Rat-SCF KL-2.";		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF01205; AAD02828.1; -.		
DR	InterPro: IPR003452; SCF.		
DR	PIRfam: PF02404; SCF; 1.		
SQ	SEQUENCE 245 AA; 27691 MW; 961511DA6AEAF82 CRC64;		

Query Match	Similarity	71.6%	Score 1000;	DB 11;	Length 245;
Best Local	Similarity	72.2%	Pred. No. 3, 2e-76;		
Matches	197;	Conservative	18;	Mismatches 30;	Indels 28; Gaps
Qy	1	MKKQTWILTCIYLQLLFLNPLVKTEIGICRNRNTNNVKDYTKLVANLPKDYMTTLKYVG	60		
Db	1	MKKQTWILTCIYLQLLFLNPLVKTEIGICRNRNTNNVKDYTKLVANLPKDYMTTLKYVG	60		
Qy	61	MDVLPFHCIMSEWVQVDSLFDLDFKFSNISGSLSNYSITDKLVIMVDVLVECVKENS	120		
Db	61	MDVLPFHCIMSEWVQVDSLFDLDFKFSNISGSLSNYSITDKLVIMVDVLVECVKENS	120		
Qy	121	KDLKSEKSEPEPRLETPPEEPRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRYST	180		
Db	121	KDYKSEKSEPEPRLETPPEEPRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRYST	180		
Qy	181	KPMPLEPVAASSLRNNSSSNRRKAKNPQGSJLHWAMALPALFSLIIGFAGALYWKK	240		
Db	175	-----KKAAPPEPDPGLQWAMALPALISLVIGFAFGALYWKK	212		
Qy	241	QPSLTRAVERNIOINEDNEISMLQEKEREQEV	273		
Db	213	QSSLTRAVERNIOINEDNEISMLQEKEREQEV	245		
RESULT	14				
ID	Q95MNS	PRELIMINARY;	PRT;	260	AA.
AC	Q95MNS				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)			
DE		STEM CELL FACTOR SHORT ISOFORM.			
OS		Mustela vison (American mink).			
OC		Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;			
OC		Mustela.			
OX		NCBI_TaxID=9667;			
RN		(11)			
RP		SEQUENCE FROM N.A.			
RA		Bennett R.D., Murphy B.D.;			
RT		"stem cell factor in the mink uterus.";			

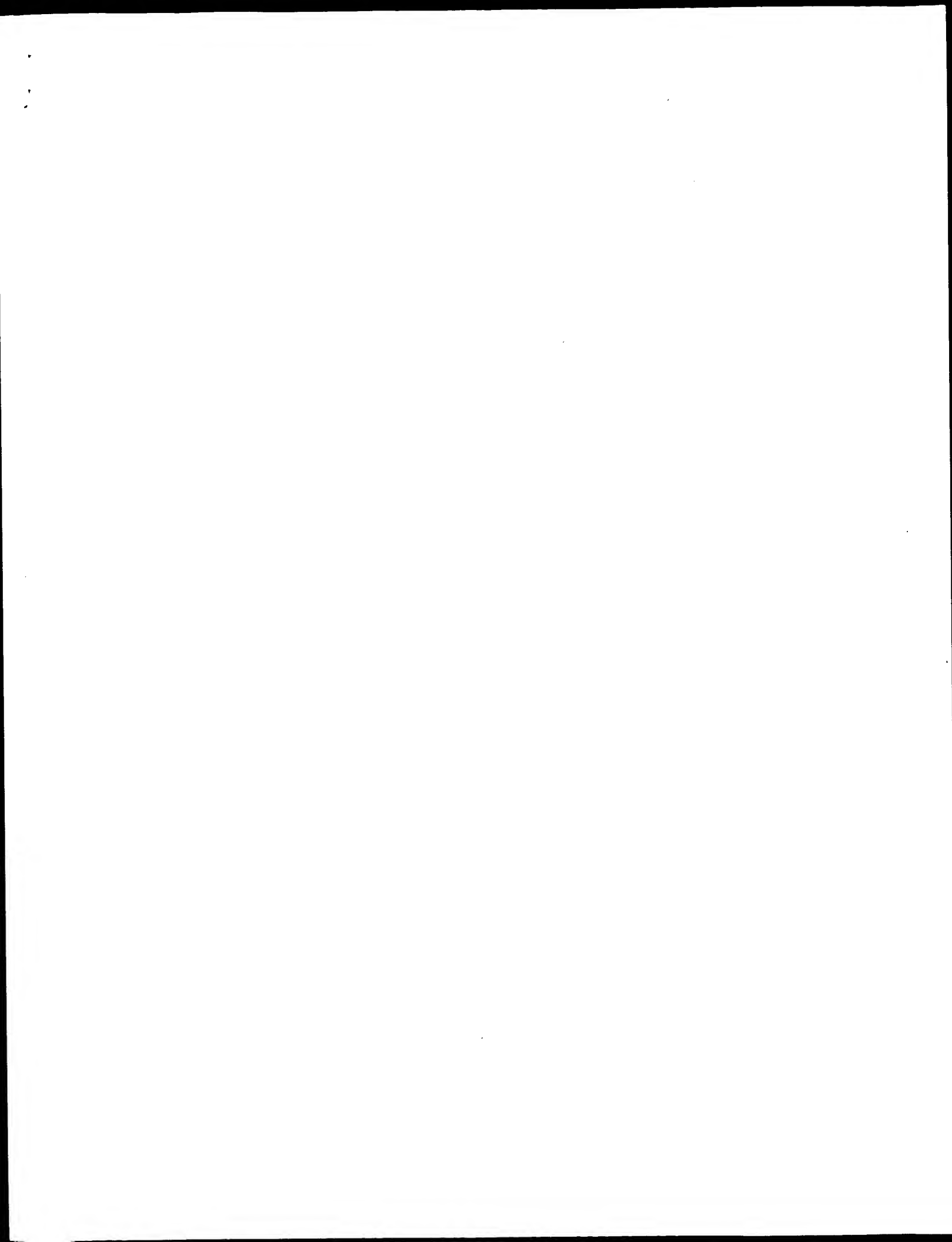
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases
DR EMBL: AF323757; AAK73366.1; -
SQ SEQUENCE 260 AA; 29542 MW; A63111CE48A50A34 CRC64;

RESULT	15		
064222			
ID	064222	PRELIMINARY:	PRT: 245 AA.
AC	064222:		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	C-KIT LIGAND TRUNCATED TRANSMEMBRANE FORM KL-2.		
GN	SL/STEEL.		
OS	Mus sp.		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10095;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92330001; PubMed=1378327;		
RA	Huang E.J., Nocka K.H., Buck J., Besmer P.;		
RT	"Differential expression and processing of two cell associated forms		
RT	of the kit-ligand: KL-1 and KL-2."		
RL	Mol. Biol. Cell 3:349-362(1992).		
DR	EMBL: S40534; AAB22555.2; -		
DR	InterPro: IPR003452; SCF.		
DR	Pfam: PF02404; SCF, 1.		
KW	Transmembrane.		
SEQUENCE	245 AA: 27541 MW; 7816113B4BD0E23B CRC64;		

```

QY 181 KPEMLPVVAASSLRNDSSSNRKAKNPPGDSLHWAMALPALESLITIGFAGALYWKRR 240
Db 175 -----KAKAPEDDSGLQITAMALPALISLYTIGFAGALYWKRR 212
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
Db 213 QSSLTRAVENIQINEEDNEISMLOEKEREFQEV 245
    
```

Search completed: August 18, 2002, 13:06:05
 Job time: 290 sec



XX (WIFE) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH,
 XX WPI: 1991-119233/17.
 DR N-PSDB; AA011543.
 XX
 PR New naturally-occurring polypeptide stem cell factor analogues -
 PR have hematopoietic biological activity of stem cell factor and
 PR are used to treat eg leukopenia, AIDS, nerve damage and
 PR infertility
 XX
 PS Disclosure; Fig 44; 127pp; English.
 XX
 CC The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AA011509-Q11543.
 CC
 XX
 SQ Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRTNNVKDVKLVANLPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnplvktegicrntnnvkdvklvanlpkdymltkyvp 60
 QY 61 MDVLPSCWISSEMYVOLSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwisemvqslsdldldkfsnseglsnysiidklvniyvdldvecvkens 120
 QY 121 KDLKSKFSKSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPEKGRKKNP 180
 DB 121 kdlkskfsksprrlftpeeffriensidaefkdfvasetsdcvssstlspekgraknp 180
 QY 181 GDSSLHMAAMALPALFSLTIGFAGALYKKRQPSLTRAVENIQINEDNEISMLQEKER 240
 DB 181 gdsslhwaamaalpalfsltigfagalyykkqpstraveniqinedneismldqeker 240
 QY 241 EFOEV 245
 DB 241 efgev 245

RESULT 2

AAR83979
 ID AAR83979 standard; Protein; 245 AA.

AC AAR83979;

DT 15-MAY-1996 (first entry)

DE Human stem cell factor derived from 5637 bladder carcinoma cell line.

XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leukopenia; AIDS; immunodeficiency; bone graft;
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.

OS Homo sapiens.

XX
 XX
 FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= sig_peptide

FT 26..245

XX /label= mat_SCF

XX EP676470-A1.

PD 11-OCT-1995.
 XX
 PF 04-OCT-1990; 90EP-0105391.
 XX
 PR 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90WO-US05548.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 XX WPI: 1995-346090/45.
 DR N-PSDB; AA104891.
 XX
 PR New stem cell factor polypeptide(s) - for stimulating the growth of
 PR primitive progenitor cells, esp. for treating disorders involving
 PR blood cells
 XX
 PS Claim 9; Fig 44; 127pp; English.

CC AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
 CC carcinoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as hematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leukopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.

XX
 SQ Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 16; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLQLLFNPVLTGEGICRNRTNNVKDVKLVANLPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnplvktegicrntnnvkdvklvanlpkdymltkyvp 60
 QY 61 MDVLPSCWISSEMYVOLSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwisemvqslsdldldkfsnseglsnysiidklvniyvdldvecvkens 120
 QY 121 KDLKSKFSKSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPEKGRKKNP 180
 DB 121 kdlkskfsksprrlftpeeffriensidaefkdfvasetsdcvssstlspekgraknp 180
 QY 181 GDSSLHMAAMALPALFSLTIGFAGALYKKRQPSLTRAVENIQINEDNEISMLQEKER 240
 DB 181 gdsslhwaamaalpalfsltigfagalyykkqpstraveniqinedneismldqeker 240
 QY 241 EFOEV 245
 DB 241 efgev 245

RESULT 3

AAU05267
 ID AAU05267 standard; Protein; 245 AA.

XX AAU05267;

XX 24-OCT-2001 (first entry)
 DT Human SCF protein isolated from the 5637 bladder carcinoma cell line.
 XX
 DE
 XX
 KW Human: stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; 5637 bladder carcinoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..25 /Label= Signal_peptide
 FT Protein 26..245 /Label= Mature_SCF
 FT Protein /Label= Mature_SCF
 XX
 PN US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982285.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI: 2001-407312/43.
 DR N-PSDB; AAS10462.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 44; 210pp; English.
 XX
 CC The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the 5637 bladder carcinoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelosclerosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency.
 CC hypopigmentation disorders i.e. plebaldism and viral induced disorders,
 CC including AIDS.
 XX
 SQ Sequence 245 AA:
 Query Match 100.0%; Score 1262; DB 22; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1,1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKKTWTWLTCTCYLQLLFNPLVKTGTCRRNRYNNKDVTKRYANLPKDYMITLKYVPG 60
 DB 1 mktgtwtlctcyqlllfnplvktgicrrnrtnnvkdvtkryanlpkdymitlkyvpg 60

OY 61 MOVLPSCWISGMVYQVLSDTLTDLDFKFSNISEGISTNSIIDKLVIYDVLVECYKENS 120
 DB 61 mdyvlpshcwisgmvyqlsdtldldfkfsniseglsntsiidklvniyddlvecykenns 120
 OY 121 KDLKSFKEPEPRLEPTPEEFERFENRSDAFKDFVVASETSQCVVSTLSSEKGRKAKPP 180
 DB 121 kdlksfkspeprlptpeeferrfnrsdafkdfvvasetsdcvvsclspekgraknpp 180
 OY 181 GDSLSHMAAMALPALFSLITGFAPGALYWKRKPSLTFRAVENIOINEDNEISMJOEKER 240
 DB 181 gdslishmaamalpalfsllitgfalgalywkrkpstlfraveniqinedneismjokek 240
 OY 241 EQGEV 245
 DB 241 eqgev 245
 RESULT 4
 AAB98368
 ID AAB98368 standard; Protein; 245 AA.
 XX
 AC AAB98368;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE Human SCF protein sequence SEQ ID NO:63.
 XX
 KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PA US6207454-B1.
 XX
 PN 27-MAR-2001.
 XX
 PD 31-DEC-1998; 98US-0224681.
 XX
 PF 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982285.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI: 2001-366062/38.
 DR N-PSDB; AAH41345.
 XX
 PT Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 PS Claim 18; Fig 44; 210pp; English.
 XX
 CC The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.

```

XX Sequence 245 AA:
SQ
Query Match
Best Local Similarity 100.0%; Score 1262; DB 22; Length 245;
Pred. No. 1.1e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRYNNKVDYTKLVANLPKDYMTITLKYPG 60
DB 1 mktktwiltciyqllefnplvktegicrnynnkvdklvankpdymtitlkypvg 60
OY 61 MDVLPSCWISSEWVQSDSLTDLDKESNISSEISNYSTIIDKLVNIVDDLVCEKENS 120
DB 61 mdvlpshcwissemvqsdsltdldkfniseglsnysiidklyniyddlvcevkens 120
OY 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKGAKNPP 180
DB 121 kdlkksfksperrlftpeeffrlnrsidafkdfvasetsdcvvsstlspekaknpp 180
OY 181 GDSSTHMAAMALPALFSIIIGFAGALYKKRROPSTLRAYENIOINEEDNEISMLQEKER 240
DB 181 gdsstlwamaalpalsiilgfaigalykkrrpsltraveniqineedneismqeker 240
OY 241 EFOEV 245
DB 241 efgev 245

RESULT 5
AAU02461
ID AAU02461 standard; Protein; 245 AA.
AC AAU02461;
XX
XX 29-AUG-2001 (first entry)
DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX
XX Human: stem cell factor; SCF: early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW 5637 bladder carcinoma.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
XX FT Protein 1..25
XX FT /label= Signal_peptide
XX FT 26..245
XX FT /label= Mature_SCF
XX
XX US6207417-B1.
XX
XX 27-MAR-2001.
XX
XX 07-JUN-1995; 95US-0482918.
XX
XX 21-DEC-1993; 93US-0172329.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (ZSEB/) ZSEBO K M.
XX (BOSS/) BOSSELMAN R A.
XX (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zsebo KM, Bossejman RA, Suggs SV, Martin FH;
XX WPI: 2001-298941/31.
XX N-PSDB: AAS04125.
DR

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XX Novel nucleic acids encoding stem cell factor useful for treating
XX disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
XX disease, kala azar, anaemia and septicemia -
XX
XX Example 5; Fig 4A-44C; 209pp; English.
XX
XX The present sequence representing human SCF (stem cell factor)
XX protein is isolated from the 5637 bladder carcinoma cell line. The
XX present invention relates to novel stem cell factors
XX (AAU02453-AAU02458, AAU02460) and the polynucleotides encoding them.
XX SCF stimulate primitive progenitor cells including early haematopoietic
XX progenitor cells. The invention also describes SCF peptides
XX (AAU02462-AAU02481) and the oligonucleotides (AAS04081-AAS04117) used
XX in the isolation of human and rat SCF sequences. The polynucleotide
XX encoding SCF is useful for producing SCF and useful in gene therapy.
XX It is useful for treating disorders involving blood cells such as
XX myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
XX Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive
XX splenomegaly, kala azar, sarcoidosis, military tuberculosis, disseminated
XX fungus disease, Fulminating septicemia, malaria, vitamin B12 and folate
XX acid deficiency, pyridoxine deficiency, and hypopigmentation disorders
XX such as piebaldism and vitiligo.
XX
XX Sequence 245 AA:
SQ
Query Match
Best Local Similarity 100.0%; Score 1262; DB 22; Length 245;
Pred. No. 1.1e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRYNNKVDYTKLVANLPKDYMTITLKYPG 60
DB 1 mktktwiltciyqllefnplvktegicrnynnkvdklvankpdymtitlkypvg 60
OY 61 MDVLPSCWISSEWVQSDSLTDLDKESNISSEISNYSTIIDKLVNIVDDLVCEKENS 120
DB 61 mdvlpshcwissemvqsdsltdldkfniseglsnysiidklyniyddlvcevkens 120
OY 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKGAKNPP 180
DB 121 kdlkksfksperrlftpeeffrlnrsidafkdfvasetsdcvvsstlspekaknpp 180
OY 181 GDSSTHMAAMALPALFSIIIGFAGALYKKRROPSTLRAYENIOINEEDNEISMLQEKER 240
DB 181 gdsstlwamaalpalsiilgfaigalykkrrpsltraveniqineedneismqeker 240
OY 241 EFOEV 245
DB 241 efgev 245

RESULT 6
AAU02767
ID AAU02767 standard; Protein; 245 AA.
AC AAU02767;
XX
XX 29-AUG-2001 (first entry)
DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX
XX Human: stem cell factor; SCF: early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW 5637 bladder carcinoma.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
XX FT Protein 1..25
XX FT /label= Signal_peptide
XX FT 26..245
XX FT Protein

```

RESULT 7

Query Match	100.0%	Score 1262;	DB 22;	Length 245;
Best Local Similarity	100.0%;	Pred. No. 11e-121;		
Matches 245; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```

QY 1 MKKTQWILTCIYLQILLFNPVLYKTEGICRNRTNNVKDYTKLVANLPKDYMITLKYPG 60
D 1 mktqtwtlctylqlllfnplvktegicrnrvtnnvkdvtklvaniipkdymltkypg 60
QY 61 MDVLPSCWISSEMYVOLSDSLTDLDKFSNISEGINSYIIDKLVNIYVDLVECVKENS 120
D 61 mdvlpshcwisemvqdsldtdldkfsniseqinsyisldklnivdvlvecvkens 120
QY 121 KDILKSKSPPEPLTPPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
D 121 kdlkksfksppepltppeefprifnrsidafkdfvvasetsdcvvsstlspekgraknp 180
QY 181 GDSSLHMAALPALFSLTIIGFAGALYWKKROPSTLRAVENIQINEDNEISMLQEKER 240
D 181 gds slhwaamalpal fsltiigfagalywkkrpsltraveniqinedneismiqeker 240
QY 241 EFQEV 245
D 241 efgev 245

RESULT 8
AAB96953 standard; Protein: 245 AA.
AC AAB96953:
DE 13-JUL-2001 (first entry)
DE Human stem cell factor SEQ ID NO: 63.
KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..25
FT Protein /label= signal_peptide
FT 26..245
FT /label= mature_stem_cell_factor

US6207802-B1.
27-MAR-2001.
09-NOV-1994; 94US-0336728.
25-NOV-1992; 92US-0982255.
16-OCT-1989; 89US-0422383.
11-JUN-1990; 90US-0537198.
24-AUG-1990; 90US-0573616.
01-OCT-1990; 90US-0589701.
(PMGE-) AMGEN INC.
Zsebo KM, Bosseiman RA, Suggs SV, Martin FH;
WPI: 2001-353108/37.
N-PSDB: AAF89105.
Novel isolated non-human mammalian stem cell factor polypeptide
stimulating growth of early haematopoietic progenitor cells, useful for
treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
sarcoidosis -
Example 5; Fig 44; 209pp; English.
The present invention provides the protein and coding sequences of
mammalian stem cell factors (SCFs). These are capable of stimulating the
growth of early haematopoietic progenitor cells, neural stem cells and

```

```

CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is an SCF described in the
CC invention.
SQ Sequence 245 AA;
Query Match 100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1,1e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLQILLFNPVLYKTEGICRNRTNNVKDYTKLVANLPKDYMITLKYPG 60
D 1 mktqtwtlctylqlllfnplvktegicrnrvtnnvkdvtklvaniipkdymltkypg 60
QY 61 MDVLPSCWISSEMYVOLSDSLTDLDKFSNISEGINSYIIDKLVNIYVDLVECVKENS 120
D 61 mdvlpshcwisemvqdsldtdldkfsniseqinsyisldklnivdvlvecvkens 120
QY 121 KDILKSKSPPEPLTPPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
D 121 kdlkksfksppepltppeefprifnrsidafkdfvvasetsdcvvsstlspekgraknp 180
QY 181 GDSSLHMAALPALFSLTIIGFAGALYWKKROPSTLRAVENIQINEDNEISMLQEKER 240
D 181 gds slhwaamalpal fsltiigfagalywkkrpsltraveniqinedneismiqeker 240
QY 241 EFQEV 245
D 241 efgev 245

RESULT 9
AA53285 standard; Protein: 246 AA.
ID AA53285
AC AA53285:
DE 27-JUL-2000 (first entry)
DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.
KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW primitive progenitor cell; haematopoietic disorder; synergic;
KW allogenic; autologous bone marrow transplant; gene therapy;
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW cancer.
OS Homo sapiens.
FH Homo sapiens.
FT Peptide 1..25
FT Protein /label= signal_peptide
FT 26..245
FT /label= mature_stem_cell_factor

US6207802-B1.
27-MAR-2001.
09-NOV-1994; 94US-0336728.
25-NOV-1992; 92US-0982255.
16-OCT-1989; 89US-0422383.
11-JUN-1990; 90US-0537198.
24-AUG-1990; 90US-0573616.
28-SEP-1990; 90US-0589701.
01-OCT-1990; 90US-0589701.
04-OCT-1990; 90EP-0310899.
(PMGE-) AMGEN INC.
Zsebo KM, Suggs SV, Bosseimann RA, Martin FH;
WPI: 2000-259135/23.
N-PSDB: AAAL3715.

```

PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -

XX Claim 23; Fig 44; 123pp; English.

CC A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.

XX Sequence 246 AA;

Query Match 99.2%; Score 1251.5; DB 21; Length 246;
 Best Local Similarity 99.6%; Pred. No. 1.3e-120;
 Matches 245; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKKTO-TWILTCYIQLDLFNPVLTGEGICRRRVNNKDYTKLVANLPKDYMTTKYVP 59
 DB 1 mkkTqtwilTcylqllfnpLvktgicrrrvnnkvdklvAnlpkdyMtlkyvp 60
 QY 60 GMDVLPSCWISBMYVQSDSLTDLDFKFSNISEGLSNYSITDKLVNIVDVLVECKENS 119
 DB 61 gmdvlpshcwisemvqvdsdsltldkfnsiseglsnysitdklvnIvddlvECKENS 120
 QY 120 SKDLKSFSPERLFTPEEFRIINRSIDAFKDFVAVASETSDCVSSTLSPEKGAKNP 179
 DB 121 skdlksfSperlftpeefrIInrsIdafkdfvAvasetScvssTlSpekgaknp 180
 QY 180 PGDSSLHMAAMALPALFSLITGFARFALYWKROPISLTRAVENTIOINEDNEISMLOEKE 239
 DB 181 pgdsslhMaamalpalFsliTgfArfAlYwkropISltraVenIoinEdneIsmlOqe 240
 QY 240 REFQEV 245
 DB 241 refgev 246

RESULT 10

AAR11711
 ID AAR11711 standard; Protein: 273 AA.

XX AAR11711;

XX 20-JUN-1991 (first entry)

XX Human Stem Cell Factor from HT1080 fibrosarcoma line.

XX Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..25

XX FT /label= sig-peptide

XX Protein 26..273

FT /label= mat-protein

XX EP423980-A.

XX 24-APR-1991.

XX 04-OCT-1990; 90EP-0310899.

XX 01-OCT-1990; 90US-0589701.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-SEP-1990; 90US-0573616.

XX 28-SEP-1990; 90MO-US05348.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH.

XX WPI; 1991-1199233/17.

XX N-PSDB; AAQ11542.

XX Disclosure; Fig 42; 127pp; English.

CC The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ11509-Q11543.

XX Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 12; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTO-TWILTCYIQLDLFNPVLTGEGICRRRVNNKDYTKLVANLPKDYMTTKYVP 60
 DB 1 mkkTqtwilTcylqllfnpLvktgicrrrvnnkvdklvAnlpkdyMtlkyvp 60
 QY 61 MDVLPSCWISBMYVQSDSLTDLDFKFSNISEGLSNYSITDKLVNIVDVLVECKENS 120
 DB 61 mdvlpshcwisemvqvdsdsltldkfnsiseglsnysitdklvnIvddlvECKENS 120
 QY 121 KDLKSFSPERLFTPEEFRIINRSIDAFKDFVAVASETSDCVSSTLSPEKGAKNP 174
 DB 121 kdLksfSperlftpeefrIInrsIdafkdfvAvasetScvssTlSpekgaknp 180
 QY 175 -----KAKNPGDSSLHMAAMALPALFSLITGFARFALYWKROPISLTRAVENTIOINEDNEISMLOEKE 212
 DB 181 kpfmlpvaasslInndsssnrkaknpPgdsSlhMaamalpalFsliTgfArfAlYwkropISltraVenIoinEdneIsmlOqe 240
 QY 213 QPSLTRAVENTIOINEDNEISMLOEKE 245
 DB 241 qpsltraVenIoinEdneIsmlOqekerefgev 273

RESULT 11

AAR20647
 ID AAR20647 standard; Protein: 273 AA.

XX AAR20647;

XX 30-APR-1992 (first entry)

Query Match 97.5%; Score 1231; DB 16; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWITLTCIYQLLFLNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 D 1 mktqtwtlctiyqlllfnpivktgicrnrvtnnvkdvklvanlpkdymitlkyypg 60

QY 61 MDVPSHCWISPMVVO/OLSDSLDLKFSNISEGINSYIIDKLVNIVDDIVECYKENS 120
 D 61 mdvpschwisemvvo/olsdsltldkfsnisegisnysliidklvniyddivecykens 120

QY 121 KDLKSKSPSPRLPTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKG----- 174
 D 121 kdlkkskspsprlptpeeffrifnrsidafkdfvasetsdcvvsstlspekgsrsvt 180

QY 175 -----KAKNPGDSSLHMAALPALFSLITIGFAFGALYWKRR 212
 D 181 kpfmlpvaaslrndsssnrkaknpgdsslhmaamalpalfslligfagalywkrr 240

QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
 D 241 qpsltravenlqneedneismloekerefev 273

RESULT 13

AAW27607
 ID AAW27607 standard; Protein: 273 AA.

AC AAW27607;

DT 28-APR-1998 (first entry)

DE Human recombinant stem cell factor protein.

XX Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.

OS Homo sapiens.

EH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein 26..274

FT /note="mature full length stem cell factor protein"

PN WO9738101-A1.

PD 16-OCT-1997.

PF 03-APR-1997; 97WO-US05541.

PR 05-APR-1996; 96US-0628428.

PA (AMGE-) AMGEN INC.

PI Lu HS;

DR WPI; 1997-512718/47.

XX Stem cell factor analogue N10D or N10D/N11D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder

PS Claim 2; Fig 1; 42pp; English.

XX This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAW27605 and AAW27606)

CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used to treat pigmentation disorders, e.g.
 CC vitilago, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitize cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.

SQ Sequence 273 AA.

Query Match 97.5%; Score 1231; DB 18; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWITLTCIYQLLFLNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60

D 1 mktqtwtlctiyqlllfnpivktgicrnrvtnnvkdvklvanlpkdymitlkyypg 60

QY 61 MDVPSHCWISPMVVO/OLSDSLDLKFSNISEGINSYIIDKLVNIVDDIVECYKENS 120

D 61 mdvpschwisemvvo/olsdsltldkfsnisegisnysliidklvniyddivecykens 120

QY 121 KDLKSKSPSPRLPTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKG----- 174

D 121 kdlkkskspsprlptpeeffrifnrsidafkdfvasetsdcvvsstlspekgsrsvt 180

QY 175 -----KAKNPGDSSLHMAALPALFSLITIGFAFGALYWKRR 212

D 181 kpfmlpvaaslrndsssnrkaknpgdsslhmaamalpalfslligfagalywkrr 240

QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245

D 241 qpsltravenlqneedneismloekerefev 273

RESULT 14

AAV53284
 ID AAV53284 standard; Protein: 273 AA.

AC AAV53284;

DT 27-JUL-2000 (first entry)

DE Human SCF protein isolated from the HRI080 fibrosarcoma cell line.

XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 KW cancer.

OS Homo sapiens.

PN EP992579-A1.

PD 12-APR-2000.

PF 04-OCT-1990; 99EP-0122861.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

PR 01-OCT-1990; 90US-0589701.

PR 04-OCT-1990; 90EP-0310899.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, BosseImann RA, Martin FH;
 XX
 DR WPI: 2000-259135/23.
 N-PSDB; AAI13714.
 XX
 PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX
 PS Claim 22; Fig 42; 123pp; English.

XX
 CC A method has been developed of making hematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining the
 CC hematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a hematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early hematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in hematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating hematopoietic disorders. The method is
 CC useful for expanding early hematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC hematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC hematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.
 XX
 SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 21; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRYTNVNVKDYTKLVANLPKDYMITLKYVP 60
 DB 1 mktqtwlitciyqllefnplvktegicrnrytnvnkvdytklvannlpkdymitlkyvp 60
 QY 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISEGLSNYSITDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwissemvylsdsltdldkfniseglsnysitdklvniyvdllvecvkens 120
 QY 121 KDLKSKFSPPRLFTPEEFERIRNRSIDAFKDFVASETSDCVYSTLSPEKG----- 174
 DB 121 kdlkskfspprlftpeeffirfnrsidafkdfvasetsdcvysstlspekdstsvst 180
 QY 175 -----KAKNPQCSLHWAMALPALFSLITGFAFGALYKKR 212
 DB 181 kpfmlpvaasslndsssnrkkpvgdssllwamaalpalfslitgafgalykkrr 240
 QY 213 QPSLTRAVENTIQINEDNEISMLQEKREPOEV 245
 DB 241 qpsltraveniqineedneismleqekerefev 273

RESULT 15
 AAU05266
 ID AAU05266 standard; Protein: 273 AA.
 XX
 AC AAU05266;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX
 KW Human: stem cell factor; SCF; hematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folate acid deficiency;
 KW hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Protein 1..25
 FT /label= Signal_peptide
 FT 26..273
 FT /label= Mature_SCF
 FT Misc-difference 97
 FT /note= "Encoded by AYT"
 FT Misc-difference 258
 FT /note= "Encoded by AYT"
 FT
 XX US6248319-B1.
 XX
 XX 19-JUN-2001.
 XX
 XX 24-MAY-1995; 95US-0449653.
 XX
 XX 10-APR-1991; 91US-0684535.
 XX 25-NOV-1992; 92US-0982255.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX 21-DEC-1993; 93US-0172329.

XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 XX Zsebo KM, BosseImann RA, Suggs SV, Martin FH;
 XX
 XX WPI: 2001-407312/43.
 DR N-PSDB; AAI10461.
 XX
 PT Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 42; 210pp; English.

XX The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the HT1080 fibrosarcoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early hematopoietic progenitor cells in human peripheral
 CC blood by administering a hematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folate acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 XX
 SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 22; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRYTNVNVKDYTKLVANLPKDYMITLKYVP 60
 DB 1 mktqtwlitciyqllefnplvktegicrnrytnvnkvdytklvannlpkdymitlkyvp 60
 QY 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISEGLSNYSITDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwissemvylsdsltdldkfniseglsnysitdklvniyvdllvecvkens 120


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QY 121 KDLKSKSPKSPPEPRLEPTPEEFPRLENRSIDAKDFVVASSETSDCVVSTLSPKSG----- 174
Db 121 kdlkksfksppeprlftpeeftrlnrsidaikdtyvasetsdcvvsstlspkdsrsvt 180
QY 175 -----KAKNPBGDSSLHWAAMALPALFSLITIGFAFGALYWKKR 212
Db 181 kpfmlpvyvaasslrndsssnrkaknpbgdsslhwaamalpalftslligfafaalYWKKR 240
QY 213 OPSTRAVENTIOINEEDNEISMLQEKEREPOEV 245
Db 241 qpslctraveniqineedneismiqekereqev 273

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Search completed: August 18, 2002, 13:08:02
 Job time: 407 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:04:01 ; Search time 41.62 seconds

(without alignments)
143,784 Million cell updates/sec

Title: US-09-604-325a-63

Perfect score: 1262

Sequence: 1 MKRTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREFGV 245

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCPUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1262	100.0	245	4	US-08-482-918-63 Sequence 63, Appl
2	1262	100.0	245	4	US-09-224-681-63 Sequence 63, Appl
3	1262	100.0	245	4	US-08-336-728A-63 Sequence 63, Appl
4	1231	97.5	273	1	US-08-220-379B-2 Sequence 2, Appl
5	1231	97.5	273	2	US-08-628-428-9 Sequence 9, Appl
6	1231	97.5	273	4	US-08-482-918-49 Sequence 49, Appl
7	1231	97.5	273	4	US-08-482-918-61 Sequence 61, Appl
8	1231	97.5	273	4	US-09-224-681-49 Sequence 49, Appl
9	1231	97.5	273	4	US-09-224-681-61 Sequence 61, Appl
10	1231	97.5	273	4	US-08-336-728A-48 Sequence 48, Appl
11	1231	97.5	273	4	US-08-336-728A-49 Sequence 49, Appl
12	1231	97.5	273	4	US-08-336-728A-61 Sequence 61, Appl
13	1231	97.5	273	4	US-08-482-918-48 Sequence 48, Appl
14	1231	97.5	273	4	US-08-482-918-50 Sequence 50, Appl
15	1231	97.5	273	4	US-08-482-918-51 Sequence 51, Appl
16	1231	97.5	273	4	US-08-482-918-52 Sequence 52, Appl
17	1231	97.5	273	4	US-08-482-918-53 Sequence 53, Appl
18	1231	97.5	273	4	US-08-482-918-54 Sequence 54, Appl
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20	1231	97.5	273	4	US-08-482-918-56 Sequence 56, Appl
21	1231	97.5	273	4	US-08-482-918-57 Sequence 57, Appl
22	1231	97.5	273	4	US-08-482-918-58 Sequence 58, Appl
23	1231	97.5	273	4	US-08-482-918-59 Sequence 59, Appl
24	1231	97.5	273	4	US-08-482-918-60 Sequence 60, Appl
25	1231	97.5	273	4	US-08-482-918-61 Sequence 61, Appl
26	1231	97.5	273	4	US-08-482-918-62 Sequence 62, Appl
27	1231	97.5	273	4	US-08-482-918-63 Sequence 63, Appl

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29	1007	79.8	273	4	US-08-482-918-53 Sequence 53, Appl
30	1007	79.8	273	4	US-09-224-681-53 Sequence 53, Appl
31	992	78.6	273	4	US-08-482-918-42 Sequence 42, Appl
32	992	78.6	273	4	US-09-224-681-42 Sequence 42, Appl
33	992	78.6	273	4	US-08-336-728A-42 Sequence 42, Appl
34	992	78.6	273	4	US-08-336-728A-54 Sequence 54, Appl
35	991	78.5	273	1	US-08-220-379B-6 Sequence 6, Appl
36	991	78.5	273	4	US-08-482-918-55 Sequence 55, Appl
37	991	78.5	273	4	US-09-224-681-55 Sequence 55, Appl
38	991	78.5	273	4	US-08-336-728A-55 Sequence 55, Appl
39	985	78.1	273	4	US-08-482-918-54 Sequence 54, Appl
40	985	78.1	273	4	US-09-224-681-54 Sequence 54, Appl
41	978	77.5	273	1	US-08-341-456A-11 Sequence 11, Appl
42	978	77.5	273	2	US-08-478-414A-11 Sequence 11, Appl
43	978	77.5	273	3	US-08-325-240A-11 Sequence 11, Appl
44	978	77.5	273	4	US-08-898-982-11 Sequence 11, Appl
45	890	70.5	208	4	US-08-836-252A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-482-918-63
Sequence 63, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosseman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESSES:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,918

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017/33005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-482-918-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKRTQWILTCIYLQLLFNPLVTEGICRRRTNNKDYTKLVANIPKDYMITLKYVPG 60
|||||

Db 1 MKKTQWILTCIYLQLLFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMVOVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
Db 61 MDVLPSCWISEMVOVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
QY 121 KDLKSKFSPEPRLPFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSSITLSPKGAKNP 180
Db 121 KDLKSKFSPEPRLPFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSSITLSPKGAKNP 180
QY 181 GDSLSLHMAAALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
Db 181 GDSLSLHMAAALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
Db 241 EFOEV 245

RESULT 2
; Sequence 63, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TRANSFER WITH STEM CELL FACTOR (SCF) POLYPEPTIDE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224, 681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005, 893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449, 653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982, 255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589, 701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573, 616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537, 198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422, 383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
Db 1 MKKTQWILTCIYLQLLFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMVOVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
Db 61 MDVLPSCWISEMVOVQSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
QY 121 KDLKSKFSPEPRLPFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSSITLSPKGAKNP 180
Db 121 KDLKSKFSPEPRLPFTPEEFRRIFNRSIDAFKDFVVASETSDCVVSSITLSPKGAKNP 180
QY 181 GDSLSLHMAAALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
Db 181 GDSLSLHMAAALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
Db 241 EFOEV 245

RESULT 3
; US-08-336-728A-63
; Sequence 63, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336, 728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982, 255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589, 701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLLFNPVLTGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLTGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
QY 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKNP 180
DB 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKNP 180
QY 181 GDSLSHMAAALPALPSLIIGFAFGALYMKRPSLTRAVENTIQINEDNEISMLQEKER 240
DB 181 GDSLSHMAAALPALPSLIIGFAFGALYMKRPSLTRAVENTIQINEDNEISMLQEKER 240
QY 241 ERFQEV 245
DB 241 ERFQEV 245

RESULT 4

US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220.379B

FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-379B-2

Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLLFNPVLTGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLTGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
QY 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKNP 180
DB 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKNP 180
QY 175 -----KAKNP GDSLSHMAAALPALPSLIIGFAFGALYMKR 212
DB 181 KFPMLPVAASSLRNDSSSNRKNRPNP GDSLSHMAAALPALPSLIIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEDNEISMLQEKEREFOEV 273

RESULT 5

US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962
GENERAL INFORMATION:
APPLICANT: Lu, Hsieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846

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REFERENCE/DOCKET NUMBER: A-400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..273
; OTHER INFORMATION: /note="NOTE: Mature full length
; OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
; OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
; OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match          97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVNVKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVNVKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISWVYVQLSDSLDLKFSNISEGLSNYSIIDKLVINYDDLVCEYKENS 120
DB 61 MDVLPSCWISWVYVQLSDSLDLKFSNISEGLSNYSIIDKLVINYDDLVCEYKENS 120
QY 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSGSVYT 180
QY 175 -----KAKNPQDSSLHMAAMALPALFSLILGFAGALYMKR 212
DB 175 -----KAKNPQDSSLHMAAMALPALFSLILGFAGALYMKR 212
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 6
US-08-482-918-49
; Sequence 49, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
```

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REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-49

Query Match          97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVNVKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVNVKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISWVYVQLSDSLDLKFSNISEGLSNYSIIDKLVINYDDLVCEYKENS 120
DB 61 MDVLPSCWISWVYVQLSDSLDLKFSNISEGLSNYSIIDKLVINYDDLVCEYKENS 120
QY 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSGSVYT 180
QY 175 -----KAKNPQDSSLHMAAMALPALFSLILGFAGALYMKR 212
DB 175 -----KAKNPQDSSLHMAAMALPALFSLILGFAGALYMKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 7
US-08-482-918-61
; Sequence 61, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
```

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-61

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVNNVADVTKLVANLPKDYMTLTKYVG 60
DB 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVNNVADVTKLVANLPKDYMTLTKYVG 60
QY 61 MDVPSHCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECYKENS 120
DB 61 MDVPSHCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECYKENS 120
QY 121 KDLSKFSKSPERLTPPEFRIRNRSIDAFKDFVAVSETSDCVVSTLSPEKGSVSVT 174
DB 121 KDLSKFSKSPERLTPPEFRIRNRSIDAFKDFVAVSETSDCVVSTLSPEKGSVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLITGFAGALYWKRR 212
DB 181 KPFMLPYVAASSLRNDSSSNRKKNPBGDSSLHMAAMALPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 8

US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/569,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVNNVADVTKLVANLPKDYMTLTKYVG 60
DB 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVNNVADVTKLVANLPKDYMTLTKYVG 60
QY 61 MDVPSHCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECYKENS 120
DB 61 MDVPSHCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECYKENS 120
QY 121 KDLSKFSKSPERLTPPEFRIRNRSIDAFKDFVAVSETSDCVVSTLSPEKGSVSVT 174
DB 121 KDLSKFSKSPERLTPPEFRIRNRSIDAFKDFVAVSETSDCVVSTLSPEKGSVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLITGFAGALYWKRR 212
DB 181 KPFMLPYVAASSLRNDSSSNRKKNPBGDSSLHMAAMALPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 9

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

```

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match          97.5%  Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%  Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

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DB 241 QPSLTRAVENTIQINEDNEISMLOEKEREFOEV 273
|||||
RESULT 10
US-08-336-728A-48
; Sequence 48, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: zeebo, Krizztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match          97.5%  Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%  Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

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Db 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKG----- 174
Db 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSRVSVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 212
Db 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 11
US-08-336-728A-49
; Sequence 49, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-728A-49

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best local similarity 89.4%; Pred No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKTQWIIITCIYQLLLFNPLVKTEGICRNVTNNVKDVKLVANLPKDYMITLKYVG 60
Db 1 MKTQWIIITCIYQLLLFNPLVKTEGICRNVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKG----- 174
Db 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKSRVSVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 212
Db 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 12
US-08-336-728A-61
; Sequence 61, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-336-728a-61

Query Match 97.5%; Score 1231; DB 4; Length 273;
 Best Local Similarity 89.4%; Pred. No. 4e-122;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQILLFNPVKTGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQILLFNPVKTGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISSEMYVQSLDSTLDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISSEMYVQSLDSTLDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGS----- 174
 DB 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 QY 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 DB 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 QY 175 -----KAKNPQDSSLHMAAMALPALFSLITGFAFGALYWKRR 212
 DB 181 KPMPLPVAASSLRNDSSSNKAKNPQDSSLHMAAMALPALFSLITGFAFGALYWKRR 240
 QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 13
 US-08-482-918-48
 Sequence 48, Application US/08482918
 Patent No. 6207417
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Krisztina M.
 APPLICANT: Bosselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,918
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 0101733005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-918-48

Query Match 97.1%; Score 1226; DB 4; Length 273;
 Best Local Similarity 89.0%; Pred. No. 1.4e-121;
 Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQILLFNPVKTGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQILLFNPVKTGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISSEMYVQSLDSTLDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISSEMYVQSLDSTLDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGS----- 174
 DB 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 QY 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 DB 121 KDLKSKSPSPRLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKGSRSVVT 180
 QY 175 -----KAKNPQDSSLHMAAMALPALFSLITGFAFGALYWKRR 212
 DB 181 KPMPLPVAASSLRNDSSSNKAKNPQDSSLHMAAMALPALFSLITGFAFGALYWKRR 240
 QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 14
 US-09-224-681-48
 Sequence 48, Application US/09224681
 Patent No. 6207454
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Krisztina M.
 APPLICANT: Bosselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
 Transfer with Stem Cell Factor (SCF) Polypeptide
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/224,681
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/005,893
 FILING DATE: 12-JAN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1226; DB 4; Length 273;
Best Local Similarity 89.0%; Pred. No. 1.4e-12;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLLFNPVTEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVTEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 180
QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIGFAGALYMKR 212
DB 181 KPEMLPPVAASSLRNDSSSNKAKNPPGSSSLHMAAMALPALFSLIGFAGALYMKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 273

RESULT 15
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zscho, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 96.3%; Score 1215; DB 4; Length 273;
Best Local Similarity 88.3%; Pred. No. 2e-120;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLLFNPVTEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVTEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 180
QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIGFAGALYMKR 212
DB 181 KPEMLPPVAASSLRNDSSSNKAKNPPGSSSLHMAAMALPALFSLIGFAGALYMKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 273

Search completed: August 18, 2002, 13:04:02
Job time: 167 sec

Sun Aug 18 14:09:05 2002

us-09-604-325a-63.rai

Page 10


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RESULT 2
A35974
mast cell growth factor precursor - human
N:Alternate names: kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35974; A61190
R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Tung, J.; Okino, K.H.; Morris, C.F.
S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
Cell 63, 203-211, 1990
A:Title: Primary structure and functional expression of rat and human stem cell factor
A:Reference number: A35974; MUID:91004219
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M59964; NID:g337933; PIDN:AAA85450.1; PID:g337934
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, I.
Cell growth Differ. 2, 373-378, 1991
A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localized
A:Reference number: A61190; MUID:9212791
A:Accession: A61190
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
C:Genetics:
A:Gene: GDB:MGP
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-273/Product: mast cell growth factor #status predicted <MCS>
F:26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <M
F:215-237/Domain: transmembrane #status predicted <TM>
F:90,97,116,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 1,9e-92;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
QY 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
DB 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRG----- 174
DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRGSVT 180
QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRG----- 174
DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRGSVT 180
QY 175 -----KAKNPPGDSLSHMAALPALSLIIGFAFGALYKKR 212
DB 181 KPFMLPYVAASSLRNDSSSNRKAANPGDSSLHMAALPALSLIIGFAFGALYKKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
RESULT 3
c-kit ligand - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
C:Accession: I46575
R:Zhang, Z.; Anthony, R.V.
Biol. Reprod. 50, 95-102, 1994
A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
A:Reference number: I46575; MUID:94146218
A:Accession: I46575

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A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <ZHA>
A:Cross-references: GB:L07786; NID:g164420; PIDN:AAA53670.1; PID:g164421
C:Superfamily: mouse mast cell growth factor
Query Match 82.2%; Score 1037.5; DB 2; Length 274;
Best Local Similarity 75.2%; Pred. No. 9.4e-77;
Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;
QY 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
DB 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRG----- 174
DB 121 ENVKSSKSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRGSVT 180
QY 175 -----KAKNPPGDSLSHMAALPALSLIIGFAFGALYKKR 211
DB 181 TRPFLPYVAASSLRNDSSSNRKAASDLSLQMAAVALPAFSLVIGFAFGALYKKR 240
QY 212 RQPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 KQPSLTRAVENTIOINEDNEISMLOEKEREFOEV 274
RESULT 4
A37934
mast cell growth factor precursor (version 2) - mouse
N:Alternate names: Kit-2 protein
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C:Accession: A37934; B43751
R:Flanagan, J.G.; Chan, D.C.; Leder, P.
Cell 64, 1025-1035, 1991
A:Title: Transmembrane form of the kit ligand growth factor is determined by alternat
A:Reference number: A37934; MUID:91160046
A:Accession: A37934
A:Molecule type: mRNA
A:Residues: 1-245 <FLA>
A:Cross-references: GB:M64262
R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the k
A:Reference number: A43751; MUID:92330001
A:Accession: A43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
A:Cross-references: GB:S04534
A:Note: the authors translated the codon TTG for residue 187 as Trp
C:Superfamily: mouse mast cell growth factor
Query Match 81.0%; Score 1022; DB 2; Length 245;
Best Local Similarity 80.8%; Pred. No. 1.5e-75;
Matches 198; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
DB 1 MKTQTWILTCIYQLLLFNPVLTGICRNRVTNNKVDYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGINSIIDLKLVNIYVDLVECKENSS 120
QY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPKRGAKNPP 180

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RESULT 6
I46929
stem cell factor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: I46929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (C-kit ligand) supports the survival of hematopoietic F
A:Reference number: I46929; MUID:93106145
A:Accession: I46929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
A:Cross-references: GB:S53329; NID:g262240; PIDN:AAB24619.1; PID:g262241
C:Superfamily: mouse mast cell growth factor

RESULT 7
 S65801
 mast cell growth factor - mouse
 N:Alternate names: hematopoietic growth factor KL, ligand steel factor; stem cell fac
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence revision 27-Feb-1997 #text change 01-Dec-2000
 C:Accession: S65801; A43751; A35976; A35977; A35972; A35975; A35973; I48768
 R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996
 A:Title: Multiple pathways for steel regulation suggested by genomic and sequence ana
 A:Reference number: S65801; MUID:97002551
 A:Accession: S65801
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <BED>
 A:Cross-references: EMBL:U044725; NID:g1172215; PIDN:AMC2447.1; PID:g1172216
 R:Huang, E.D.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the k
 A:Reference number: A43751; MUID:92330001
 A:Accession: A43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-214, 'L', '216-273 <HUA>
 A:Cross-references: GB:S40364; NID:g251668; PIDN:AMB22554.2; PID:g5705957
 A:Note: the authors translated the codon TTG for residue 215 as Trp
 R:Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Le
 Cell 63, 225-233, 1990
 A:Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the lig
 A:Reference number: A35976; MUID:91004221
 A:Accession: A35976
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', 208-270 <HUT>
 A:Cross-references: GB:M38511
 R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; Mar
 Cell 63, 233-243, 1990
 A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active
 A:Reference number: A35977; MUID:91004223
 A:Accession: A35977
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <AND>
 A:Cross-references: GB:A57647; GB:M38436; NID:g199151; PIDN:AAA39538.1; PID:g199152
 R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.U.; Jenkins, N.A.; Cosman, D.;
 Cell 63, 175-183, 1990
 A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and
 A:Reference number: A35972; MUID:91004216

A:Accession: A35972
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 26-53 <COP>
 A:Cross-references: GB:M59912
 R:Zebedo, K.M.; Williams, D.A.; Geissler, E.N.; Brody, V.C.; Martin, F.H.; Atkins, H.L.;
 Catalanach, B.M.; Gall, S.J.; Suggs, S.V.
 Cell 63, 213-224, 1990
 A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
 A:Reference number: A35975; MUID:91004220
 A:Accession: A35975
 A:Molecule type: mRNA
 A:Residues: 1-201 <2SE>
 A:Cross-references: GB:M59915; NID:9200935; PIDN:AAA0095.1; PID:9554271
 R:Zebedo, K.M.; Wypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
 A.; Langley, K.E.
 Cell 63, 195-201, 1990
 A:Title: Identification, purification, and biological characterization of hematopoietic
 A:Reference number: A35973; MUID:91004218
 A:Accession: A35973
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-29, 'R', 31-39 <2S2>
 R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
 Genes Dev. 6, 1832-1842, 1992
 A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect in t
 A:Reference number: A44071; MUID:93012940
 A:Accession: 148768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', 208-273 <RES>
 A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PID:9395284
 C:Genetics:
 A:Gene: SLF
 A:Map position: 10
 A:Superfamily: mouse mast cell growth factor
 C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 78.5%; Score 991; DB 2; Length 273;
 Best Local Similarity 72.2%; Pred. No. 5.5e-73;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;
 QY 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 DB 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENAP 120
 QY 121 KDLKSKFSPERLFTPEEFRIFNRSIDAFKDFVAVSEFSDCVVSTLSPK 174
 121 KDLKSKFSPERLFTPEEFRIFNRSIDAFKDFVAVSEFSDCVVSTLSPK 174
 DB 121 KDLKSKFSPERLFTPEEFRIFNRSIDAFKDFVAVSEFSDCVVSTLSPK 180
 QY 175 -----KAKNPQDSSILHMAAMALPALFSLITGFAGALYMKR 212
 175 -----KAKNPQDSSILHMAAMALPALFSLITGFAGALYMKR 212
 DB 181 KPEMLPVAASSLRNDSSSNRKAAPEDSGIOWTAMALPALISLVIGFAGALYMKR 240
 QY 213 QPSLTRAVENTIQINEDNEISMLQEKEREFQY 245
 213 QPSLTRAVENTIQINEDNEISMLQEKEREFQY 245
 DB 241 QSSLTRAVENIQINEDNEISMLQEKEREFQY 273

RESULT 8
 S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.

A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:9940807; PIDN:CAA90620.1; PID:9940808
 C:Superfamily: mouse mast cell growth factor

Query Match 59.4%; Score 749.5; DB 2; Length 202;
 Best Local Similarity 83.9%; Pred. No. 1.5e-53;
 Matches 146; Conservative 15; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 DB 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENHSF 120
 QY 121 KDLKSKFSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPK 173
 121 KDLKSKFSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPK 173
 DB 121 ENVKSSKSPERLFTPEEFRIFNRSIDAFKDFELVASTMSECVYSTSPK 174

RESULT 9
 S35974
 stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris,
 S.J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev
 Cell 63, 203-211, 1990
 A:Title: Primary structure and functional expression of rat and human stem cell facto
 A:Reference number: A35974; MUID:91004219
 A:Accession: B35974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA4211.1; PID:9554507
 R:Lu, H.S.; Clogeton, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zse
 J. Biol. Chem. 266, 8102-8107, 1991
 A:Title: Amino acid sequence and post-translational modification of stem cell factor
 A:Reference number: A39805; MUID:91217037
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: E', 27-190 <LUN>
 C:Superfamily: mouse mast cell growth factor

Query Match 57.1%; Score 721; DB 2; Length 201;
 Best Local Similarity 79.8%; Pred. No. 3e-51;
 Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 DB 1 MKKTOWITTCIYQLLFFNPVKTGECICRNRYNNKVDYTKLVANLPKDYMTLTKYVG 60
 QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDVLVECKENAP 120

RESULT 10
 S70367
 stem cell factor short form precursor - quail

Sun Aug 18 14:09:06 2002

us-09-604-325a-63.rpt

1

2

3

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:02:07 ; Search time 35.93 Seconds

(Without alignments)
264.021 Million cell updates/sec

Title: US-09-604-325a-63

Perfect score: 1262

Sequence: 1 MKKTQWILTCIYLQILLEN.....NEEDNEISMLQEKEREFQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	1231	97.5	273	1 SCF_HUMAN	P21583 homo sapien
2	1037.5	82.2	274	1 SCF_PIG	Q02030 sus scrofa
3	1014.5	80.4	274	1 SCF_CANFA	Q06220 canis famli
4	991	78.5	273	1 SCF_MOUSE	P20826 mus musculu
5	721	57.1	201	1 SCF_RAT	P21581 rattus norv
6	584	46.3	287	1 SCF_CHICK	Q09108 gallus gall
7	97	7.7	482	1 T2PA_YEAST	P36100 saccharomyc
8	94.5	7.5	403	1 RAGE_MOUSE	Q63151 mus musculu
9	91	7.2	378	1 FDHA_METVA	Q64959 rattus norv
10	91	7.2	402	1 RAGE_RAT	Q64959 rattus norv
11	91	7.2	981	1 SCF4_RICPE	Q64959 rattus norv
12	90.5	7.2	1675	1 POL_RIBVP	Q64959 rattus norv
13	90	7.1	267	1 PRL_NPVH	P21583 homo sapien
14	90	7.1	411	1 RMOG_CHLBN	Q02030 sus scrofa
15	89	7.1	2238	1 RRP1_BUNTW	Q06220 canis famli
16	88	7.0	447	1 DNAA_SYNX3	Q06220 canis famli
17	87.5	6.9	966	1 CAPP_MEDSA	P20826 mus musculu
18	87.5	6.9	1175	1 SRS2_YEAST	P21581 rattus norv
19	87	6.9	664	1 ZARA_CAEEL	Q09108 gallus gall
20	86.5	6.9	370	1 NREF_HAELN	P36100 saccharomyc
21	86.5	6.9	2492	1 TALA_DICDI	Q63151 mus musculu
22	86	6.8	469	1 C39A_HUMAN	Q64959 rattus norv
23	86	6.8	1146	1 KMAA_DICDI	Q64959 rattus norv
24	85	6.7	804	1 SUS2_ARATH	Q64959 rattus norv
25	85	6.7	953	1 UURA_RICPR	Q64959 rattus norv
26	85	6.7	1188	1 PRSA_METVA	Q64959 rattus norv
27	84.5	6.7	466	1 DNAA_PROMI	Q64959 rattus norv
28	84.5	6.7	1075	1 CAPP_TOBAC	Q64959 rattus norv
29	84.5	6.7	1075	1 PST2_SCHPO	Q64959 rattus norv
30	84.5	6.7	2156	1 RPL_HUMAN	Q64959 rattus norv
31	84	6.7	935	1 COGQ_YEAST	Q64959 rattus norv
32	84	6.7	935	1 W31_YEAST	Q64959 rattus norv
33	84	6.7	1224	1 MSN5_YEAST	Q64959 rattus norv

34	84	6.7	1522	1 BA13_HUMAN	Q60242 homo sapien
35	83.5	6.6	456	1 DNAL_CHLTR	Q64252 chlamydia t
36	83.5	6.6	796	1 DECI_YEAST	Q12387 saccharomyc
37	83.5	6.6	830	1 EP2_DICDI	P15112 dictyostell
38	83.5	6.6	998	1 SCA4_RICAK	Q941X9 rickettsia
39	83.5	6.6	1742	1 MYSC_HUMAN	Q941X9 rickettsia
40	83	6.6	989	1 PTP3_DICDI	Q941X9 rickettsia
41	83	6.6	1584	1 BA11_HUMAN	Q941X9 rickettsia
42	82.5	6.5	425	1 YNU7_YEAST	Q941X9 rickettsia
43	82.5	6.5	450	1 DNAA_SPICI	Q941X9 rickettsia
44	82.5	6.5	451	1 DNAA_PASMT	Q941X9 rickettsia
45	82.5	6.5	463	1 DNAA_PROSS	Q941X9 rickettsia

ALIGNMENTS

RESULT 1	SCF_HUMAN	STANDARD:	PRT:	273 AA.
ID	P21583			
AC	P21583			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
DE	cell growth factor) (MGF).			
GN	Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91004219; PubMed=2208279;			
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,			
RA	Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,			
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,			
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,			
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.,			
RT	"Primary structure and functional expression of rat and human stem cell factor DNAs."			
RL	Cell 63:203-211(1990).			
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.			
CC	-1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.			
CC	-1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.			
CC	-1- SIMILARITY: BELONGS TO THE SCF FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: M59964; AA85450.1; -			
DR	PIR: A35974; A35974.			
DR	MIM: 184745; -			
DR	InterPro: IPR003452; SCF.			
DR	Pfam: PF02404; SCF.1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.			
FT	SIGNAL	1	25	
FT	CHAIN	26	273	KIT LIGAND.
FT	DOMAIN	26	214	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	215	237	POTENTIAL.
FT	DOMAIN	238	273	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	29	114	BY SIMILARITY.

FT DISULFID 68 163 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB39C6607 CRC64;

Query Match 97.5%; Score 1231; DB 1; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2.4e-91;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYQLLLFNPLVTEGICRNRYNNKYDKLVANLPKDYMTTLKYVG 60
 DB 1 MKKTQWIIITCIYQLLLFNPLVTEGICRNRYNNKYDKLVANLPKDYMTTLKYVG 60
 QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKSEKSPERLFTPEEFERIFNRSIDAFKDFVVASSETSDCVYSTLSPEKRG----- 174
 DB 121 KDLKSEKSPERLFTPEEFERIFNRSIDAFKDFVVASSETSDCVYSTLSPEKRG----- 180
 QY 175 -----KAKNPPGSSSLHWAAMALPALESLIIGFAFGALYWKRR 212
 DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGSSSLHWAAMALPALESLIIGFAFGALYWKRR 240
 QY 213 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 245
 DB 241 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 273

RESULT 2

SCF_PIG 2
 ID SCF_PIG STANDARD; PRT; 274 AA.

AC 029030:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Sus scrofa (Pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;
 RX MEDLINE=94146218; PubMed=7508758;
 RA Zhang Z., Anthony R.V.;
 RT "Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";
 RL Biol. Reprod. 50:95-102(1994).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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CC EMBL; L07786; AAA53670.1; -
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF; 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT CHAIN 26 274 KIT LIGAND.
 FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 216 238 POTENTIAL.
 FT DISULFID 239 274 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 29 114 BY SIMILARITY.
 FT DISULFID 68 164 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 274 AA; 31118 MW; F53C8711AD7BA666 CRC64;

Query Match 82.2%; Score 1037.5; DB 1; Length 274;
 Best Local Similarity 75.2%; Pred. No. 6.7e-76;
 Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

QY 1 MKKTQWIIITCIYQLLLFNPLVTEGICRNRYNNKYDKLVANLPKDYMTTLKYVG 60
 DB 1 MKKTQWIIITCIYQLLLFNPLVTEGICRNRYNNKYDKLVANLPKDYMTTLKYVG 60
 QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKSEKSPERLFTPEEFERIFNRSIDAFKDFVVASSETSDCVYSTLSPEKRG----- 174
 DB 121 KDLKSEKSPERLFTPEEFERIFNRSIDAFKDFVVASSETSDCVYSTLSPEKRG----- 180
 QY 175 -----KAKNPPGSSSLHWAAMALPALESLIIGFAFGALYWKRR 211
 DB 181 KPFMLPVAASSLRNDSSSNRKAASDSIEDSSLOMAAVALPAFSLVIGFAFGALYWKRR 240
 QY 212 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 245
 DB 241 KQNLTRVAVNIQUINEDNEISMLOEKEREFOEV 274

RESULT 3

SCF_CANFA 3
 ID SCF_CANFA STANDARD; PRT; 274 AA.

AC 006220:
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedes; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=93106145; PubMed=1261786;
 RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W., Martin F.H.;
 RT "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture.";
 RL Exp. Hematol. 20:1118-1124(1992).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC or send an email to license@isb-sib.ch).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S53329; AAB24619.1; -
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF. 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 274
 FT TRANSMEM 26 215
 FT DOMAIN 216 238
 FT DISULFID 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 SQ SEQUENCE 274 AA; 30869 MW; 4182BBAED0073B CRC64;

Query Match 80.4%; Score 1014.5; DB 1; Length 274;
 Best Local Similarity 74.8%; Pred. No. 4.6e-74;
 Matches 205; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKKTQWILTCITQLLLFNPVKTEGICNRNTNNKVDYTKLVANLPKDYMTLKYVPG 60
 Db 1 MKKTQWILTCITQLLLFNPVKTEGICNRNTNNKVDYTKLVANLPKDYMTLKYVPG 60
 QY 61 MDVLPSCWISWVAVQSLVSLTDLKFSNISGLSNYSITDKLVNIVDDLYECVKNSS 120
 Db 61 MDVLPSCWISWVAVQSLVSLTDLKFSNISGLSNYSITDKLVNIVDDLYECVKNSS 120
 QY 121 KDLKSKSPERPLTPPEEFRRFNSSDAKDF-VVASETSDCVVSSFLSPKRG----- 174
 Db 121 ENVKKAPKSPKLPPEEFRRFNSSDAKDF-VVASETSDCVVSSFLSPKRG----- 180
 QY 175 -----KAKNPQDSSLHMAAMALPALFSLITIGFAGALYMKK 211
 Db 181 TKPFMLPVAASLRLNDSSSNKASNSIGDSNLOMAAMALPFRFSLVIGFAGALYMKK 240
 QY 212 ROPSULRAVENIOINEDNEISMLOEKEREFOEV 245
 Db 241 KOPNLRTVENIOINEDNEISMLOEKEREFOEV 274

RESULT 4
 SCF_MOUSE STANDARD: PRT; 273 AA.
 AC P20826;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF) (Hematopoietic growth factor KL) (KL-1
 DE protein) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=WCB6F1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
 RA Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
 RA Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that
 RT is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 RT of the kit-ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=WCB6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by
 RT alternative splicing and is missing in the Sld mutant.";
 RL Cell 64:1025-1035(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
 RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
 RA Copeland N.G.;
 RT "Developmental abnormalities in Steel17H mice result from a splicing
 RT defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for Steel regulation suggested by genomic and
 RT sequence analysis of the murine Steel gene.";
 RL Genetics 142:927-934(1996).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=102/ELX3H/EL1; TISSUE=Brain;
 RA Gray J.;
 RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 RT the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233(1990).
 RN [8]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murodock D.C.,
 RA Jacobsen P.W., Langley K.E., Smith K.A., Takeshita T., Cattanech B.M.,
 RA Galli S.J., Sugas S.V.;
 RT "Stem cell factor is encoded at the Sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [9]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [10]
 RP PARTIAL SEQUENCE OF 26-78.

RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene."
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY
 CC THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN
 CC VARYING RATIOS IN DIFFERENT TISSUES.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE
 CC ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR
 CC DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; M59915; AAA40095.1; -;
 DR EMBL; M57647; AAA39538.1; -;
 DR EMBL; X68989; CAA48778.1; -;
 DR EMBL; U44724; -; NOT_ANNOTATED_CDS.
 DR EMBL; U44725; AAC52447.1; -;
 DR EMBL; X95381; CAA64667.1; -;
 DR EMBL; S40364; AAB2554.2; -;
 DR EMBL; M59912; AAA39539.1; -;
 DR PIR; A35971; A35971.
 DR PIR; A35972; A35972.
 DR PIR; A35975; A35975.
 DR PIR; A35976; A35976.
 DR PIR; A35977; A35977.
 DR PIR; A43751; A43751.
 DR PIR; B35971; B35971.
 DR MGI; MGI:96974; KIL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal;
 KW Alternative splicing; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 26 273
 FT DOMAIN 26 214
 FT TRANSMEM 215 237
 FT DOMAIN 238 273
 FT DISULFID 29 114
 FT DISULFID 68 163
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 195 195
 FT VARSPDLIC 175 202
 FT VARIANT 207 207
 FT VARIANT 215 215
 FT CONFLICT 215 215
 FT SEQUENCE 273 AA; 30645 MW; A7FC899B592A7967 CMC64;

Query Match 78.5%; Score 991; DB 1; Length 273;
 Best Local Similarity 72.2%; Pred. No. 3.4e-72;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

1 MKKTQWILTCIYLLLFNPLVKTGICRNRVNNVADVTKLVAANLFRDKYITLKYYPG 60

DB 1 MKKTQWILTCIYLLLFNPLVKTGICRNPVTDVNDVKDTFLVAAANPNDYMITLNVAG 60
 OY 61 MDVLPSHCWISENVYQSDSLTDLDFNSISELSNYSITIDKLVNVYDVLVEKRNSS 120
 DB 61 MDVLPSHCWLDNVYIQLSLTTLDFKSNISELSNYSITIDKLVYDVLVDMENAP 120
 OY 121 KDIKFSKSPERLFTPEEPFRINRSIDAFKDPVVASETSDCVSSTLSPKSG----- 174
 DB 121 KNIKSPRPETRSTFTPEEFSTNRSDADKDPVWASDTSDCVLSSTLGPCKSRVSVT 180
 OY 175 -----KAKNPPGSSLHWAMALPALPSLITGRFALYKKR 212
 DB 181 KPFLMPVVAASSLRNDSSSSNRKAKAPEDSGLOMTAMALPALISLYIGFAFGALYKKR 240
 OY 213 OPSLTRAVENTIQINEDNEMISMLQEKREPOEV 245
 DB 241 OSLLTRAVENTIQINEDNEISMLOOKEREPOEV 273
 RESULT 5
 SCF_RAT STANDARD: PRT: 201 AA.
 AC P21581;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MCF) (Fragment).
 GN KITLG OR MGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91004219; PubMed=2208279;
 RA Morris F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
 RA Martin C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
 RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
 RA Fisher E.F., Ertavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
 RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
 RT "Primary structure and functional expression of rat and human stem
 RT cell factor DNAs."
 RL Cell 63:203-211(1990).
 RN [2]
 RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC STRAIN=BUFAIO; TISSUE=Liver;
 RX MEDLINE=91217037; PubMed=1108771;
 RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
 RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
 RT "Amino acid sequence and post-translational modification of stem cell
 RT factor isolated from buffalo rat liver cell-conditioned medium."
 RL J. Biol. Chem. 266:8102-8107(1991).
 RN [3]
 RP SEQUENCE OF 26-39.
 RX MEDLINE=91004218; PubMed=2208278;
 RA Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
 RA Karkare S.B., Sachdev R.K., Yushchenko V.N., Birkett N.C.,
 RA Williams L.R., Satyagal V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
 RA Langley K.E.;
 RT "Identification, purification, and biological characterization of
 RT hematopoietic stem cell factor from buffalo rat liver-conditioned
 RT medium."
 RL Cell 63:195-201(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.


```

CC      -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; M59966; AAA42117.1; -.
CC      PIR; B35974; B35974.
CC      PIR; A35973; A35973.
CC      InterPro; IPR003452; SCF.
CC      Pfam; PF02404; SCF. 1.
CC      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC      FM SIGNAL 1 25
CC      FM CHAIN 26 >201 KIT LIGAND.
CC      FM MOD_RES 26 26 PYROLIDONE CARBOXYLIC ACID.
CC      FM DISULFID 29 114
CC      FM CARBOHYD 68 163
CC      FM CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PARTIAL).
CC      FM CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
CC      FM CARBOHYD 167 167 O-LINKED (PROBABLE).
CC      FM CARBOHYD 168 168 O-LINKED (PROBABLE).
CC      FM CARBOHYD 180 180 O-LINKED (PROBABLE).
CC      FM CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (PARTIAL).
CC      FM NON_TER 201
CC      SEQUENCE 201 AA; 22537 MW; 188868C1DA4F21B CRC64;

Query Match 57.1%; Score 721; DB 1; Length 201;
Best Local Similarity 79.8%; Pred. No. 8.5e-51;
Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILICIVYLLFNPLVKTGICRNRYNNVNDVYKLVANLPRDVIITLKYPG 60
DB 1 MKKTQWILICIVYLLFNPLVKTGICRNRYNNVNDVYKLVANLPRDVIITLKYPG 60
QY 61 MDVLPSCWISSENVVOLSLSLTLDFKFSNISSEGLSNYSIIDKLVNIYDDLEVCYKENS 120
DB 61 MDVLPSCWISSENVVOLSLSLTLDFKFSNISSEGLSNYSIIDKLVNIYDDLEVCYKENS 120
QY 121 KDLKRSKSPERLTPPEPFRIENRSDIAFDVASTSPCVVSTLSPK 173
DB 121 KDLKRSKSPERLTPPEPFRIENRSDIAFDVASTSPCVVSTLSPK 173
QY 121 KNNKESLAKRETNPTEPFRIENRSDIAFDVASTSPCVVSTLSPK 173
DB 121 KNNKESLAKRETNPTEPFRIENRSDIAFDVASTSPCVVSTLSPK 173

RESULT 6
SCF_CHICK
ID SCF_CHICK STANDARD: PRT; 287 AA.
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MCF).
GN KITLG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93737344; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES.

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```

CC      PROBABLY INTERLEUKINS.
CC      -----
CC      -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC      SECRETED SOLUBLE FORM.
CC      -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; D13516; BAA02733.1; -.
CC      PIR; JN0637; JN0637.
CC      InterPro; IPR003452; SCF.
CC      Pfam; PF02404; SCF. 1.
CC      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC      FM SIGNAL 1 25
CC      FM CHAIN 26 287 KIT LIGAND.
CC      FM MOD_RES 26 225 EXTRACELLULAR (POTENTIAL).
CC      FM DISULFID 226 246 POTENTIAL.
CC      FM DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
CC      FM DISULFID 29 117 BY SIMILARITY.
CC      FM CARBOHYD 68 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FM CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FM CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FM CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      SEQUENCE 287 AA; 32328 MW; 6A8556AD0C152578 CRC64;

Query Match 46.3%; Score 584; DB 1; Length 287;
Best Local Similarity 44.6%; Pred. No. 1.1e-39;
Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;

QY 1 MKKTQWILICIVYLLFNPLVKTGICRNRYNNVNDVYKLVANLPRDVIITLKYPG 60
DB 1 MKKTQWILICIVYLLFNPLVKTGICRNRYNNVNDVYKLVANLPRDVIITLKYPG 60
QY 61 MDVLPSCWISSENVVOLSLSLTLDFKFSNI--SEGLSNYSIIDKLVNIYDDLEVCYK 117
DB 61 MDVLPSCWISSENVVOLSLSLTLDFKFSNI--SEGLSNYSIIDKLVNIYDDLEVCYK 117
QY 118 NSKSD-LKRSKSPERLTPPEPFRIENRSDIAFDVASTSPCVVSTLSPK 175
DB 118 NSKSD-LKRSKSPERLTPPEPFRIENRSDIAFDVASTSPCVVSTLSPK 175
QY 121 KNNKESLAKRETNPTEPFRIENRSDIAFDVASTSPCVVSTLSPK 173
DB 121 KNNKESLAKRETNPTEPFRIENRSDIAFDVASTSPCVVSTLSPK 173
QY 176 -----AKNP-----GDSLHMAMALPAFLSLIG 201
DB 176 -----AKNP-----GDSLHMAMALPAFLSLIG 201
QY 202 FAFGALYMKKROP-SITRAVENIQIN--EDNEISMLQEKREFOEV 245
DB 202 FAFGALYMKKROP-SITRAVENIQIN--EDNEISMLQEKREFOEV 245
QY 241 FIFGALYMKKTHPKSPRESNETIQCHGQENETSMQLQKREHLQY 287
DB 241 FIFGALYMKKTHPKSPRESNETIQCHGQENETSMQLQKREHLQY 287

RESULT 7
T2EA_YEAST
ID T2EA_YEAST STANDARD: PRT; 482 AA.
AC P36100;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription initiation factor IIF, alpha subunit (TIF1E-alpha)
DE (Transcription factor A large subunit) (Factor A 66 kDa subunit).
GN TFI1 OR YKL028W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)

```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-71; 102-108 AND 206-220.
 RC STRAIN-Bj926;
 RX MEDLINE=95050500; PubMed=7961670;
 RA Feaver W.J., Henry N.L., Bushnell D.A., Sayre M.H., Brickner J.H.,
 RA Gileadi O., Kornberg R.D.,
 RT "yeast TFEII. Cloning, expression, and homology to vertebrate
 RT proteins";
 RL J. Biol. Chem. 269:27549-27553(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rieger M.,
 RL Submitted (MAR-1994) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: RECRUITS TFIIF TO THE INITIATION COMPLEX AND STIMULATES
 CC THE RNA POLYMERASE II C-TERMINAL DOMAIN KINASE AND DNA-DEPENDENT
 CC ATPASE ACTIVITIES OF TFIIF. BOTH TFIIF AND TFEII ARE REQUIRED FOR
 CC PROMOTER CLEARANCE BY RNA POLYMERASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: STRONG, TO MAMMALIAN TFEII-ALPHA.
 CC
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 CC
 CC EMBL: U12825; AAA62665.1; -
 DR EMBL: Z28028; CAA81863.1; -
 DR PIR: S37845; S37845.
 DR TRANSFAC: T02239; -
 DR SGD: S0001511; TEAL.
 DR InterPro: IPR002853; TFEII_alpha.
 DR Pfam: PF02002; TFEII_alpha.1.
 DR SMART: SM00531; TFEII_alpha.1.
 DR Transcription regulation; Nuclear protein; Zinc-finger.
 KW ZN_FING 124 152
 FT DOMAIN 374 482 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 374 392 POLY-GLU
 FT DOMAIN 374 392
 FT SEQUENCE 482 AA; 34742 MW; 3E789DFC4247EF8A CRC64;
 SO
 Query Match 7.7%; Score 97; DB 1; Length 482;
 Best Local Similarity 18.4%; Pred. No. 1.6;
 Matches 54; Conservative 53; Mismatches 89; Indels 98; Gaps 11;
 QY 12 IYQLLEFNPLVKTGICRNRVTNNVADYTKLVANLKRQVITL----- 55
 DB 27 IYLDALFHSYLAEDDL-KOLLSTINKTELGLPLARLSDRLSLHKOREYPPNSKSVERY 85
 QY 56 ----RYVPGMDVLPSPHCW-ISEMVVQLSDSLTD-----LDDKFSNI----- 91
 DB 86 YYYVYPAIDAIR---KWYQVQVRLKDDLDKNSPEWGPCICLRYTQLEAVQLNF 142
 QY 92 -----SEGLSNTSIDKLNYVDLVECV-----KENSMDLKKSRSP 130
 DB 143 DRTFELCSLDEPLEVDEDSGKKNKEDKRLNKLMDQIPIIDSLTKIDSDISENTEIEIA 202
 QY 131 ERLTTPPEFFRIFNRSIDAFKDFVVASSETSCVSVSTLSPEKGRKAKNPDDSSLHMAAM 190
 DB 203 IARLIPQ-----NOSHAA-----TYNKKSGSTMRPPDSA----- 234
 QY 191 ALPAFLSLTIGFAGALYWKKROPSLTRAVENTIOINEDNETISMLQEKREFOE 244
 DB 235 PLPNTLMGTALGDS-----SRAGANSQATLTIINTTASDEVAQRELEQROAE 283
 RESULT 8
 RAGE_MOUSE STANDARD: PRT; 403 AA.
 AC 062151:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Advanced glycosylation end product-specific receptor precursor
 DE (receptor for advanced glycosylation end products).
 GN AGER OR RAGE.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunn E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RT in normal and diabetic rats";
 RL Mol. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL: L33412; AAA40040.1; -
 DR MGD: MGI:893592; Ager.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003598; Iq_C2.
 DR InterPro: IPR003600; Iq_Like.
 DR Pfam: PF00047; Iq; 3.
 DR SMART: SM00410; Iq_Like; 1.
 DR SMART: SM00408; IqC2; 1.
 DR PROSITE: PS00290; Iq_MHC; 1.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 403
 FT DOMAIN 23 341
 FT TRANSMEM 342 362
 FT DOMAIN 363 403
 FT DOMAIN 31 105
 FT DOMAIN 136 213
 FT DOMAIN 251 307
 FT DISULFID 38 98
 FT DISULFID 143 207
 FT DISULFID 143 300
 FT CARBOHYD 25 25
 FT CARBOHYD 80 80
 FT SEQUENCE 403 AA; 42668 MW; 1279796FD1579357 CRC64;
 SO
 Query Match 7.5%; Score 94.5; DB 1; Length 403;
 Best Local Similarity 26.0%; Pred. No. 2.1; Indels 45; Gaps 7;
 Matches 39; Conservative 19; Mismatches 47; Indels 45; Gaps 7;
 QY 112 VECVKNSSKDLKSEKSPRLTFPEPRIFRNSIDAFKDFVASE-TSDCVSSTLS 170
 DB 268 VHWIKDCAPLPL-----APSPVLLLEPVGH-----ADEGYSCVAT---H 304
 QY 171 PEKGRANP-----GDSSLHMAAMALPAFLSL-IIGFAGALYWK 211
 DB 305 PSHGPQSPSPVSIWETGDEGPAEGSVGSGLTALALGILGAGVALLGAILMK 364

QY 212 ROP--SLFRANENIQINEDNEISWLOKE 239
 DB 365 RQPRREKRAKAPESQDEEBERALNOSDAE 394

RESULT 9
 FDHA_METJA
 ID FDHA_METJA STANDARD; PRT; 378 AA.
 AC 060314:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative formate dehydrogenase alpha chain (EC 1.2.1.2).
 GN MJO006.
 OS Methanococcus jannaschii.
 OC Archaea: Euryarchaeota: Methanococcales; Methanococcaceae;
 CC Methanococcus.
 OK NCBI_TaxID=2190;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kiehlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weisskopf K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Harte M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- CATALYTIC ACTIVITY: Formate + NAD(+) = CO(2) + NADH.
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN), ZINC, FAD. MAY BIND A 4FE-4S
 CC CLUSTER (BY SIMILARITY).
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U67459; AAB97987.1; -.
 DR HSSP: P07658; IAA6.
 DR TIGR: M00006; -.
 DR InterPro: IPR001467; Molybdopterin.
 DR Pfam: PF00384; molybdopterin.2.
 DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
 DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
 DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
 KW Hypothetical protein; Oxidoreductase; Zinc; Flavoprotein; Molybdenum;
 KW FAD; NAD; Iron-sulfur; 4Fe-4S; Complete proteome.
 FT METAL 8 8 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 11 11 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 15 15 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 43 43 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SEQUENCE 378 AA; 42050 MW; EDC13060FF2609AA CRC64;

Query Match 7.2%; Score 91; DB 1; Length 378;
 Best local similarity 21.7%; Pred. No. 3.7;
 Matches 64; Conservative 29; Mismatches 82; Indels 120; Caps 15;

QY 12 IYQLLENPVTEG-----ICRNRYNVKQV-----K 42
 DB 53 IYHERKPKFLIKKNGKLVETWDEALSFIAKLNKYNADITITAGSKCTNEDNVALKK 112

QY 43 LV-----ANLPK-----DYMITLKYVGR-----DYLPSCHWISSEWVOLSDS 80
 DB 113 LVDSLAKAKIGHCICNSPRVNTAEVSTTIIDIEAKNIIITIGDFSEHALIGRRVIAKKE 172
 QY 81 LTDL-----LDKF-----SNISSEGLSNYS-----IIDKLVNIVDLVECVKE 117
 DB 173 GSKVTIFNTEERKEILKLNADFEKVDVSYLGVDLSNVDKNTIIINAPVN-VDEIITAKE 231
 QY 118 NSSKDL--KSKFSPERL-----FTPEEFFRIFNNS-----IDAFK--DF 154
 DB 232 NKAQVLPAKACNTVGATLIGIPALNDEYFELKSKFLYINGENPALVDKDKLVKNEF 291
 QY 155 VV-----ASETSDCVSVSTLSPEK-----GKAKNPQDSSLHW 187
 DB 292 LVYQDIIMETFAEMADVYVLPSTCAEMKDFITMDRIKRIKAVNPQDAMDW 346

RESULT 10
 PAGE_RAT
 ID PAGE_RAT STANDARD; PRT; 402 AA.
 AC 063495;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Advanced glycosylation end product-specific receptor precursor
 DE (Receptor for advanced glycosylation end products).
 GN AGER OR RAGE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautler M.P., Nagashima M., Lundh E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautler J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RT in normal and diabetic rats.";
 RL MOL. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: U33413; AAA42027.1; -.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003600; IG_Like.
 DR Pfam: PF000477; Ig; 3.
 DR SMART: SM00410; IG_Like; 1.
 DR SMART: SM00408; IG_C2; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 402 ADVANCED GLYCOSYLATION END PRODUCT-
 FT DOMAIN 23 341 SPECIFIC RECEPTOR.
 FT TRANSMEM 342 362 EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.

FT DOMAIN 363 402 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 31 105 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 212 212 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 250 306 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 143 98 POTENTIAL.
 FT DISULFID 257 296 POTENTIAL.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 402 AA; 42663 MW; 594481HC3A51E94E CRC64;

Query Match 7.2%; Score 91; DB 1; Length 402;
 Best Local Similarity 27.3%; Pred. No. 4;
 Matches 36; Conservative 12; Mismatches 46; Indels 38; Gaps 5;

OY 129 SPEERLFTPEEFFRIFNRSIDAFKDFVASETSDCVSSTLSPKGRKNP----- 180
 DB 279 APSVYLLPE-----VGHDEGITYSCVATHPSHGQESPVNIRVTER 321
 OY 181 GD-----SSLHMANALPLFLSL-IIGFAPGLYKKRPSL--TRAVENIOINE 227
 DB 322 GDEGQAGSVYDGSGLGTALALGILGGLAALLIGAILMKRKPRLERKAPESODEE 361
 OY 228 EDNEISMJOEKE 239
 DB 382 ERAELNOSSEAE 393

RESULT 11
 SCA4_RICE STANDARD; PRT; 981 AA.
 AC 09A37; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
 DE (Protein PS 120) (Fragment).
 CN SCA4 OR D.
 OS Rickettsia felis (Rickettsia azadi).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
 OX NCBI_TaxID=42862;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Sekyova Z., Roux V., Raoult D.;
 RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
 RT gene D coding for an intracytoplasmic protein.";
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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 CC
 DR EMBL; AF196973; AAK31304.1; -
 KW Antigen.
 FT NON_TER 1
 FT NON_TER 981
 SQ SEQUENCE 981 AA; 107514 MW; 7F18F421E2C262E1 CRC64;

Query Match 7.2%; Score 91; DB 1; Length 981;
 Best Local Similarity 25.1%; Pred. No. 12;
 Matches 48; Conservative 24; Mismatches 59; Indels 60; Gaps 10;
 OY 19 ENFLVTEGICRNRVTNNVKD-----VTKLIVANLPKDYMITLKYVGM-DV 63
 DB 628 ENTIKTEAI--QNTTKYLDSPKRAIGETLESTIKYVASSPLNGDOKADIVAGMGA 685

OY 64 LPSH-----CWISMVVOQLSDSLFDLDK-----FSNISEGLSNYSI----- 100
 DB 666 IASHSTMAPTKEKISTSTSEVEKGVASTITDLEDKLMTKGLVGEIGKANPEITSEKTA 745
 OY 101 ----IDKLIVNYVD--LVECKE-----NSSKDIK-SEKSPERPLFTPEEFFRIF 144
 DB 746 VSRGIDKSTALPEDEKQALKDANEAALDRETQNLTEGILKRONLGEPPKPR-----DDIYNKA 801
 OY 145 NSISAFKDFV 155
 DB 802 QDVADALKNVI 812

RESULT 12
 POL_RTBVP STANDARD; PRT; 1675 AA.
 AC P27502; P27528; 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Polypeptide (P194 protein) [contains: Coat protein; Protease
 DE (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Ribonuclease H
 DE (EC 3.1.26.4)].
 OS Rice tungro bacilliform virus (isolate Philippines) (RTBV).
 OC Viruses; Retroid viruses.
 OX NCBI_Taxid=10655;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91252204; PubMed=2041739;
 RA Hay J.M., Jones M.C., Blakebrough M.L., Dasgupta I., Davies J.W.,
 RA Hull R.;
 RT "An analysis of the sequence of an infectious clone of rice tungro
 RT bacilliform virus, a plant pararetrovirus.";
 RL Nucleic Acids Res. 19:2615-2621(1991).
 RN 12
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 503-526.
 RX MEDLINE=92024093; PubMed=1926781;
 RA Ou R.D., Bhattacharya M., Laco G.S., de Kochko A., Rao B.L.S.,
 RA Kanlewska M.B., Elmer J.S., Rochester D.E., Smith C.E.,
 RA Beachy R.N.;
 RT "Characterization of the genome of rice tungro bacilliform virus:
 RT comparison with Cornelina yellow mottle virus and caulimoviruses.";
 RL Virology 185:354-364(1991).
 CC -1- SIMILARITY: WITH COMELINA YELLOW MOTTLE VIRUS POLYPROTEIN, AND
 CC WITH CAULIMOVIRUSES ORF V.
 CC -1- SIMILARITY: WITH RETROVIRAL POL/GAG POLYPROTEINS.
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 CC
 DR EMBL; X57924; CAA40997.1; -
 DR EMBL; M65026; AAB03094.1; -
 DR PIR; C40785; C40785.
 DR MEROPS; A03.002; -
 DR InterPro: IPR001995; Asp.prol.retrov.
 DR InterPro: IPR001969; Asp.protease.
 DR InterPro: IPR000477; RTase.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam; PF00077; rvp; 1.
 DR Pfam; PF00078; rvt; 1.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR SMART; SM00343; ZnF_C2HC; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR Polyprotein; RNA-directed DNA polymerase; Hydrolyase;
 KW Aspartyl protease; transferase; Nucleotidyltransferase; Coat protein;
 KW Endonuclease; Zinc-finger.

FT CHAIN 503 ? 33 KDA COAT PROTEIN.
 FT 2N_FLING 772 789 POTENTIAL.
 FT ACT_SITE 987 987 PROTEASE (BY SIMILARITY).
 FT CONFLICT 1292 1292 D->E (IN REF. 2).
 FT CONFLICT 1630 1630 Y->H (IN REF. 2).
 FT CONFLICT 1635 1635 S->P (IN REF. 2).
 FT SEQUENCE 1675 AA; 194081 MW; B24D7181463E466F CRC64;

Query Match
 Best Local Similarity 25.6%; Pred. No. 25;
 Matches 56; Conservative 35; Mismatches 87; Indels 41; Gaps 12;

35 NNKQVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVOLDSITLIDLFPS-----N 90
 1362 NKKVEGCVLSK--KSKMFLKEVEYLG-----EIKGKISLOPHIVDIKFKDKNKN 1414
 91 ISEGISNT-SIIDKLVNIYVDLVECVKENSCKDKSKFSKSEPRFTPEEFPRIF--NRS 147
 1415 TLKGLQAVTLGINTARGYIKDKSLV-----GPLYKKTGKNGO-RIFNKEEDMIIFKIERE 1469
 148 IDAFKDFVAVSETSDCVVSTLSPEKGRKKNPGRDSSLHMAAAL--PALFS-----LI 200
 1470 VSKIPLEPRKET-DYIILETDASEEG-----WGAVLVCKPKDKYSGKTEKIA 1516
 201 GFAPGALYWKRRKPSLTRAVENTIQINEDNEISMLOEKE 239
 1517 GYASGNFGEKKTMTSLDYEIE--AINELANKFOIYLDKD 1553

RESULT 13

PK1_NPVHZ
 ID PK1_NPVHZ STANDARD; PRT; 267 AA.

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Serine/threonine-protein kinase 1 (EC 2.7.1.1).
 GN PK1 OR PK-1.
 OS Heliothis zea nuclear polyhedrosis virus (HsNPV) (Helicoverpa zea single nucleocapsid nuclear polyhedrosis virus)
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 ON NCBI_TaxID=28290;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ELKAR;
 RA Tribe D., Bulach D.M., Goodge K., Robertson A.P.S., Wu T., Lee H., McAdams A., Cowan P.J.;
 RL Submitted (OCT-1994) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ELKAR;
 RA MEDLINE=97321796; PubMed=9178498;
 RA Le T.H., Wu T., Robertson A.P.S., Bulach D.M., Cowan P.J., Goodge K., Tribe D.;
 RT "Genetically variable triplet repeats in a RING-finger ORF of Helicoverpa species baculoviruses";
 RL Virus Res. 49:67-77(1997).
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES.

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CC EMBL, L36721; AAA50302.1; -
 DR HSP; 067264; AAB54091.1; -
 DR HSP; P05132; ICRP.

DR InterPro: IPR000719; Elk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP, FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST, 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM, 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 18 266
 FT NP_BIND 24 32
 FT BINDING 47 47
 FT ACT_SITE 134 134
 FT SEQUENCE 267 AA; 31531 MW; DIFB332CEC16AD53 CRC64;

Query Match
 Best Local Similarity 7.1%; Score 90; DB 1; Length 267;
 Matches 50; Conservative 34; Mismatches 78; Indels 54; Gaps 11;

37 VKDYTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVOLDSITLIDLFPSNISEG 94
 54 VTELEPLVHQLMKDNRFFIKLY--SLTTLKSQLILIDYVA--GDDLFPFLKHKKYSVA 109
 95 LSNSIIDKLVNIYVDLVECVKENSCKDKSKFSKSEPRFTPEEFPRIF--RIFNS 147
 110 -ETRSIVGQLFEALNAL-----HSYKTIHNDKLENLVYRRKQIYLDYGLCKIVNTS 162
 148 I--DAFKDFVAVSETSDCVVSTLSPEKGRKKNPGRDSSLHMAAALPALFSITIGFAG 205
 163 SCRDGTKEY-----MSPEKLRQN--YDVHVMWALGI-LTYELLIGH--- 202
 206 ALYKKRRKPSLTRAVENTIQINEDNEISMLOEKERE 241
 203 -----HPKHSNDEEDFDLDVLOQRQK 226

RESULT 14

RMUC_CHLPN
 ID RMUC_CHLPN STANDARD; PRT; 411 AA.

DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA recombination protein rmuc homolog.
 GN RMUC OR CPN0982 OR CP0874.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxID=83358;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RA MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lamell C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RA MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Uitterback T., Berry K., Bass S., Liner K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Morn and Chlamydia pneumoniae Ar39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RA MEDLINE=20330349; PubMed=10871362;
 RA Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

```

RT      "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT      from Japan and CM1029 from USA."
RL      Nucleic Acids Res. 28:2311-2314(2000).
CC      -1- FUNCTION: Involved in DNA recombination (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE RMOC FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AE001678; AAD19119.1; -.
DR      EMBL: AE002246; AAF38663.1; -.
DR      EMBL: AF002548; BAA9189.1; -.
DR      TIGR: CP0874; -.
DR      InterPro: IPR003798; DUF195.
DR      Pfam: PF02646; DUF195.1.
KW      DNA recombination; Coiled coil; Complete proteome.
FT      DOMAIN 26 64 COILED COIL (POTENTIAL).
FT      DOMAIN 123 143 COILED COIL (POTENTIAL).
SQ      SEQUENCE 411 AA; 47020 MW; 976E6EC1708581E CRC64;

Query Match
Best Local Similarity 7.1%; Score 90; DB 1; Length 411;
Matches 45; Conservative 33; Mismatches 56; Indels 44; Gaps 9;

QY      71 SEMVYQSDSLTDLDFKFSNISEGLSNYSITIDKLVNYVDLVEGVKNSKDLKSP-RS 129
DB      195 ADIIRLPEQDRCLITDKAPISDSYFVEIDK-GDLVDKIKKIKKIKLKKSTWEKPHOS 253
QY      130 PE-PRLEFPEPEFRIFNKSIDAFKDFVVASSETSDCVSYSTLSPEKGRKKNPPGSSILHMA 188
DB      254 PEYIILFPGF--SLFNDAIRLAPLMEIGASSNVIILSPLE----- 293
QY      189 AMALPALFSLIIGFAGALYKKRPPSLTRAVENTIOINEEDNEISML-QEKEREFOEV 245
DB      294 --LIALIKTYI-----AYMKWQ-----ENIQ-KQIQEVSLLGKELHRLQVY 331

RESULT 15
RRPL_BUNYW STANDARD; PRT: 2238 AA.
ID RRPL_BUNYW
AC P20470;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Bunyamwera virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Bunyavirus.
OX NCBI_TaxID=11573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085791; PubMed=2596023;
RA Elliott R.M.;
RT "Nucleotide sequence analysis of the large (L) genomic RNA segment of
RT Bunyamwera virus, the prototype of the family Bunyaviridae.";
RL Virology 173:426-436(1989).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

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DR      EMBL: X14383; CAA32553.1; -.
DR      PIR: A33744; RRYUBY.
DR      Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
SQ      SEQUENCE 2238 AA; 258668 MW; 1ED00AB156BAC8DA CRC64;

Query Match
Best Local Similarity 7.1%; Score 89; DB 1; Length 2238;
Matches 70; Conservative 41; Mismatches 108; Indels 108; Gaps 17;

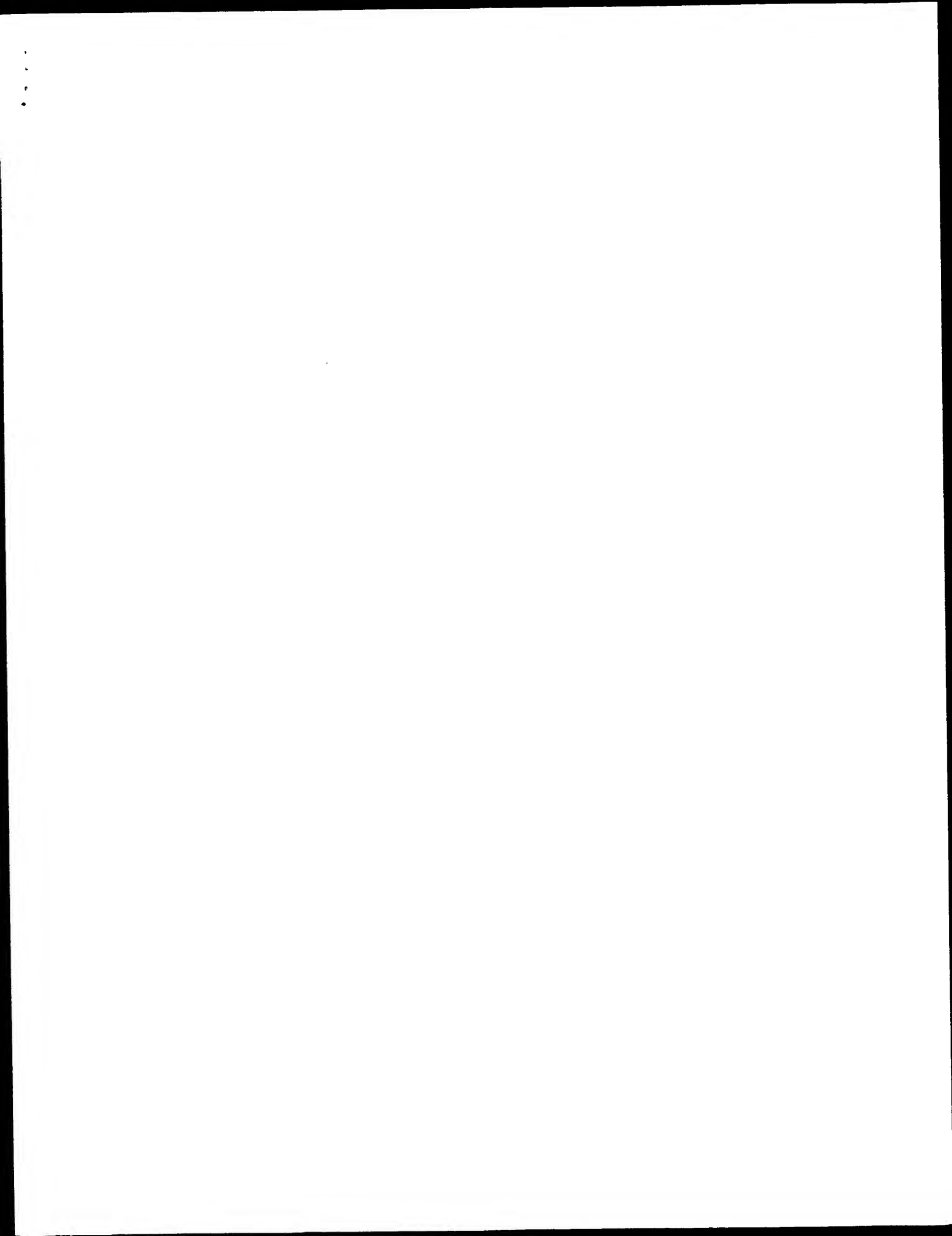
QY      2 KKOTWILTCIYLQDLLFNP-----LVKTEG-----ICRNRYTN 35
DB      1064 EKTRILYMCNVMQKLLIPDDLJANILDDQKRPYNDLLEMTGLNRYVVOIKRMVLOG 1123
QY      36 NKVDYTKLVANLPKDYMTTLKYV--PGNDVLPSCWISSEMYQSDSLTDLDFKFSNISE 93
DB      1124 NFNYISSYVHSCA--MLVYKDILKECKMLDGGCLNSM-VHSDDKOTSL-----AIIQN 1175
QY      94 GLSNYSITIDKLVNYVDLVEGVKNSKDLKSPKSPPEPLTPDEFFRIFN--RSIDA 150
DB      1176 KVSDDIVQYANNTPEVY--CLTEGCGANMKKTYIT-----HTCKEFVSLFNHGEPLSV 1228
QY      151 FKDFVVASSETSDCV-----VSTLSPEKGRKAN--PGDSSILHMAAMA----- 191
DB      1229 FGRFLIPS-VGDCAYIGPYEDLASRLSAQOSLKRKCPP--SLWLAISCSHWITFTTY 1284
QY      192 -----LPAFLSLIIGFAGALYV-----KKRPS 215
DB      1285 NMLDDQINAPQOHLFPNNRKEIPVELNGYLNAPFLIINLVGLGNNLFLNLIKRVLP- 1343
QY      216 LTRAVENTIOIN--EEDNEISMLQEKER 240
DB      1344 LDKOKETIQSOCLHLNCSIDKLTLESEK 1370

Search completed: August 18, 2002, 13:02:08
Job time: 53 sec

```

Sun Aug 18 14:09:06 2002

us-09-604-325a-63.rsp



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:06:05 ; Search time 114.11 Seconds

(without alignments)

Title: US-09-604-325A-63
Perfect score: 1000

sequence: 1 MKKTQTWILTCIYLQLLFN.....NEEDNEISMLQEKEREFEQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 562222 seqs, 172994929 residues

total number of hits satisfying chosen parameters: 562222

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

```

database : sptrembl_19:*
1: sd arches:*

```

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1:  sp.archaea:*
SPRMBL_19:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrata:*
6:  sp.mammal:*
7:  sp.mmc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.verticillate:*
14: sp.unclassified:*
15: sp.rvms:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1249	99.0	245	4	Q9UQK7	Q9UQK7 homo sapien
2	1051.5	83.3	274	6	P79169	P79169 felis silve
3	1031	81.7	245	11	Q9Z2E7	Q9Z2E7 rattus nor
4	1022.5	81.0	260	6	Q9SMN5	Q9SMN5 mustela vis
5	1021.5	80.9	274	6	Q9SM15	Q9SM15 capra hircu
6	1018.5	80.7	274	6	Q28132	Q28132 bos taurus
7	1014.5	80.4	274	6	Q9SN18	Q9SN18 mustela vis
8	1009	80.0	245	11	Q64222	Q64222 mus sp. c-h
9	992	78.6	273	11	Q9QWZ4	Q9QWZ4 rattus nor
10	991	78.5	273	11	Q62524	Q62524 mus muscul
11	991	78.5	273	11	Q921N5	Q921N5 mus muscul
12	990.5	78.5	267	6	P79368	P79368 ovis aries
13	990	78.4	273	11	P97332	P97332 mus muscul
14	988.5	78.3	261	6	Q9SM22	Q9SM22 equus cabal
15	951.5	75.4	256	6	O62765	O62765 equus cabal
16	715	56.7	208	11	Q64384	Q64384 mus muscul

17	605	47.9	253	13	Q90315	Q90315	coturnix co
18	583	46.2	287	11	Q90314	Q90314	coturnix co
19	509	40.3	123	11	Q61854	Q61854	mus musculut
20	339	26.9	271	13	Q9YGP2	Q9YGP2	ambystoma m
21	282	22.3	54	4	Q16487	Q16487	homo sapien
22	265.5	21.0	96	6	Q95MG8	Q95MG8	equus cabal
23	223.5	17.7	47	6	Q95MG7	Q95MG7	equus cabal
24	136	10.8	36	6	Q9U774	Q9U774	bos taurus
25	109	8.6	937	10	Q9M14	Q9M14	arabidopsis
26	102.5	8.1	919	10	Q9LPD8	Q9LPD8	arabidopsis
27	102.5	8.1	1498	3	Q9P884	Q9P884	emeritella
28	102.5	8.1	1498	3	Q96VK6	Q96VK6	emeritella
29	102	8.1	1501	3	Q96VL9	Q96VL9	botrytis cl
30	100.5	8.0	51	6	Q9N1Y5	Q9N1Y5	equus cabal
31	99	7.8	539	12	Q91H18	Q91H18	discua des
32	97.5	7.7	402	11	Q95444	Q95444	mus muscului
33	97	7.7	1447	16	Q9P0J8	Q9P0J8	ureaplasma
34	94.5	7.5	1515	3	Q96VK4	Q96VK4	emeritella
35	93.5	7.4	576	11	Q62970	Q62970	rattus norv
36	93.5	7.4	647	16	Q98BP9	Q98BP9	mycoplasma
37	93.5	7.4	3227	3	Q13834	Q13834	schizosach
38	93	7.4	1298	10	Q9L5A4	Q9L5A4	arabidopsis
39	93	7.4	1962	10	Q9P6T2	Q9P6T2	arabidopsis
40	93	7.3	512	16	Q9GCA7	Q9GCA7	lactococcus
41	92.5	7.3	534	5	Q21299	Q21299	caenorhabdi
42	92	7.3	420	16	Q980M8	Q980M8	mycoplasma
43	92	7.3	821	16	Q92E65	Q92E65	listeria in
44	91.5	7.3	1993	5	P90670	P90670	aplysia cal
45	91	7.2	317	5	Q9VY12	Q9VY12	drosophila

ALIGNMENTS

RESULT	1			
090UK7				
ID	090UK7	PRELIMINARY;	PRT;	245 AA.
AC	090UK7;			
DT	01-MAY-2000 (TRENBLREL, 13, Created)			
DT	01-MAY-2000 (TRENBLREL, 13, Last sequence update)			
DT	01-DEC-2001 (TRENBLREL, 19, Last annotation update)			
DE	STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99160429; PubMed=10049787;			
RA	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;			
RT	"Parathyroid hormone-regulated production of stem cell factor in human			
RL	osteoblasts and osteoblast-like cells.";			
RL	Biochem. Biophys. Res. Commun. 255:778-784(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han C., Peng X., Yuan J., Qiang B.;			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF119835; AAD22048.1; -;			
DR	EMBL; AF400437; AAK92486.1; -;			
DR	InterPro; IPR003452; SCF.			
DR	Pfam; PF02404; SCF.1.			
SQ	SEQUENCE 245 AA: 27903 MW: F887983163A3C36 CRC64;			

Query Match	99.0%;	Score 1249;	DB 4;	Length 245;
Best Local Similarity	98.8%;	Score 1248;	DB 4;	Length 245;

Matches	242;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
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[illegible]

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Query Match Similarity      83.3%: Score 1051.5; DB 6; Length 274;
Best Local Similarity      76.6%: Pred. No. 9.4e-82;
Matches 210; Conservative 17; Mismatches 18; Indels 29; Gaps 2

QY      1 MKKTQWIIITCIYIQLLENNPLVKTGEGICRNRVTNNVKDVTKIYANLPKDIYMITLKYVYG 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1 MKKTQWIIATCIYIQLLENNPLVKTGICRNRFTDVKDVTKIYANLPKDIYKIALKYVYG 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 MDVLPFHCHTISEMYVQSLSDIIDLKFGNISFCGLSNYSITDKLVNIYDVLVYCCKENS 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       61 MDVLPFHCHTISYVEQSLSLTDLDRFSITSGLSNYSITDKLVNIYDVLVYCVCCHSS 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121 KDLKSKFSKSEPRLPFPPEEFRIJFNSIDAFAKDF-VVASETSDCVVYSTLSPEKG----- 174
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       121 ENVKSSKSEPRLPFPPEEFRIJFNSIDAFAKDFLEWYASKTSCEVYSTLSPEKDSRVSY 180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      175 -----KANNPDDSSLIHMAAMLPLPLSLITIGFAFGALYWK 211
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       181 TKDFMLPVAASSLRLNDSSSNRKANIPLEDSSIQWAVMALPACFSVLVIFAFAGFYWK 240
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      212 RQPSLTRAVERNIOINEEDNEISMLOEKEREFQEV 245
        : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       241 KQPNLRTYVENIQINEEDNEISMLOEKEREFQEV 274
        : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      3
ID          Q9Z2E7
AC          Q9Z2E7;
DT          01-MAY-1999 (TEMBLrel. 10, Created)
            01-MAY-1999 (TEMBLrel. 10, Last sequence update)

```

Query Match	Similarity	81.7%	Score 1031	Da 11	Length 245:
Best Local	198	Conservative	18	Mismatches	29
Matches				Indels	0
				Gaps	0
QY	1	MKKTQWILTCIYLQLLLENNPLVKTEGICRNRVTNNVKQVTKLVANLPMQWITLLKYNG	60		
Db	1	MKKTQWITTCIYLQLLLENNPLVKTEGICRNRVTNNVKQVTKLVANLPMQWITLLKYNG	60		
QY	61	MDVLPSCWISSEWVQVDSFLDLDKFSNISSEGLSNYSIIDLKYNIVDLYECYKENS	120		
Db	61	MDVLPSCWISSEWVQVDSFLDLDKFSNISSEGLSNYSIIDLKYNIVDLYECYKENS	120		
QY	121	KDLKSKFSKPEPLFTPEEFERFENSDIAKQFVYASFSQCVYASTSPSEKGRKNPP	180		
Db	121	KDKSKFSKPEPLFTPEEFERFENSDIAKQFVYASFSQCVYASTSPSEKGRKNPP	180		
QY	181	GDSSLWMAAMALPALPSLIIGFAFGALYMKRQPSLTRAVENTQINEEDNETSMLOEKR	240		
Db	181	EDPGLOMTAMALPALPSLIIGFAFGALYMKRQPSLTRAVENTQINEEDNETSMLOEKR	240		
QY	241	ERQEV	245		
Db	241	ERQEV	245		

RESULT	4	
Q95MN5		
ID	Q95MN5	PRELIMINARY; PRT; 260 AA.
AC	Q95MN5	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)	
DE	STEM CELL FACTOR SHORT ISOFORM.	
OS	Mustela vison (American mink).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;	
OC	Mustela.	
OX	NCBI_TaxID=9667;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Bennett R.D., Murphy B.D.: "Stem cell factor in the mink uterus."	
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.	
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.	
SR	EMBL: AF232357; AAK73366.1; -	
SQ	SEQUENCE 260 AA; 29542 MW; A63111C448A50A34 CRC64;	

Query Match	81.0%	Score 1022.5	DB 6	Length 260
Best Local Similarity	80.7%	Pred. No. 2.6e-79		
Matches 197	Conservative	22	Mismatches 24	Indels 1
				Gaps 1
QY	1	MKKQTMVLTTCYIQLLEFNPLVKTGICRRRVYNNVKDYTKLVANLPKDYMITLKYVPG	60	
		: : : : : : : : : :		
		: : : : : : : : :		
Db	1	MKKQTMVLTTCYIQLLEFNPLVKTGICRRRVYNNVKDYTKLVANLPKDYMITLKYVPG	60	
QY	61	MDVPSHCWISSEMYVQSDSLTDLDKFSNTSEGISYNSYIDKLVTNIVDLDVECKENSS	120	

Query Match	80.0%	Score 1009	DB 11	Length 245
Best Local Similarity	80.4%	Pred. No. 3	4e-78	
Matches 197	Conservative 19	Mismatches 29	Indels 0	Gaps 0
QY	1	MKKQTWTLLTCIYVQLLLFFNPLVTEGICGNRRVYNNKYADYTKLVANIPKDYMTLEKYYVG	60	
Db	1	MKKQTWTLLTCIYVQLLLFFNPLVTKRKCICGNPVDYNNKDTTKLVANIPNDYMTLEKVVAG	60	
QY	61	MDVLPSPHCWISSEMYVQDSLSLTDLDDFFNSISEGLSNYSITLDKLVNIIVDDLVCEVKNSS	120	
Db	61	MDVLPSPHCWMLNDWYIQSLSTLTFLDDKFNISISEGLSNYSITLDDKIGKIVDDLVLCMEENAP	120	
QY	121	KDLKSKFSPPERRLFTPEPEFFRINRSDIAFKPDVYVASESDCVASSTLSPEKGAKKANP	180	
Db	121	KNIKSKSPRPETRSTPEEPFSINRSDIAKDDWYASDTSDCVLSSTLTPEKGAKKANP	180	
QY	181	GDSSLHWAMALPALFSLITIGFAEGALYWKRRQDSTLTRAVENTQINEDNEISMLDEKER	240	

	Query Match	78.6%;	Score 992;	DB 11;	length 273;	
	Best Local Similarity	71.8%;	Pred. No. 1.le-76;			
	Matches 196;	Conservative 18;	Mismatches 31;	Indels 28;	Gaps 1	
QY	1 MKKTOTWITTCIYIOLLFNFLVTEGICRNRVTNNKVYTKLVANLPKDMITLKAVPG 60	: : : : :				
Dd	1 M KKTOMITTCIYIOLLFNFIYVKIQICNPATDVKQKITLVANLNDNYITLLNTAVAG 60	: : : : :				
QY	61 MYIPSHOCISMVYVOUSDLTDLDFKFSISGLSNYSIIIRLVNIYDDLDVECEKNSS 120	: : : : :				
Dd	61 MDVLPSHCLRMVTHLSVS LTTLLDFKFSISGLSNYSIIDRLGKIYDDLDVACKEENAP 120	: : : : :				
QY	121 KDCLKSEKSPERLTPPEEFRTINRSIDAKPQFVAASESQCVSSTSPESPKG----- 174	: : : : :				
Dd	121 KNVKESLKKPETRNPTPEEFPFSIFNRSIDAKPMAASDTSDCVLSTTIGPAKDSRVST 180	: : : : :				
QY	175 -----KAKNPPGDSSLHMAAMALPALFSLTIJAFAGALYMKRR 212	: : : : :				
Dd	181 KPMLLPVVAASSLRDSSSRKAASKAASPEDPGLOWTAMALPALISDIYIGFAFGALYMKRK 240	: : : : :				
QY	213 QPSLTRAVENIOINEDNEIMSLQKEEPDEPV 245	: : : : :				
Dd	241 QSSTRAVENIOINEDNEIMSLQKREPEDEV 273	: : : : :				

RESULT	10		
ID	062524	PRELIMINARY;	PRT; 273 AA.
AC	062524:		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	MAST CELL GROWTH FACTOR.		
GN	KITL OR MGF.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/EL. TISSUE=BRAIN.		
RC	MEDLINE=97032534; PubMed=8875993;		
RA	Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.,		

"Molecular analysis of two new Steel mutations in mice shows a RT transversion or an insertion."
 RT Mamm. Genome 7:843-846(1996).
 DR EMBL: X99322; CA67698.1; -.
 DR MGD: MGI:96974; KIL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF, 1.
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA: 30645 MW: B3E9D0B72C734107 CRC64;

Query Match 78.5%; Score 991; DB 11; Length 273;
 Best Local Similarity 72.2%; Pred. No. 1.3e-76;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNRVNNKVDYKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNPVDNDVITKLVANLPNDYMITLNYAG 60
 QY 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 212
 DB 181 KPFMLPPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWKRR 240
 QY 213 QPSLTRAVENTIQUEDNEISMLQEKEREFQEV 245
 DB 241 QSSLTRAVENTIQUEDNEISMLQEKEREFQEV 273

RESULT 11
 ID Q921N5 PRELIMINARY; PRT; 273 AA.
 AC Q921N5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SIMILAR TO KIT LIGAND.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC013322; AAH1322.1; -.
 SQ SEQUENCE 273 AA: 30661 MW: A7FC91E3939320107 CRC64;

Query Match 78.5%; Score 991; DB 11; Length 273;
 Best Local Similarity 72.2%; Pred. No. 1.3e-76;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNRVNNKVDYKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNPVDNDVITKLVANLPNDYMITLNYAG 60
 QY 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174

QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 212
 DB 181 KPFMLPPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWKRR 240
 QY 213 QPSLTRAVENTIQUEDNEISMLQEKEREFQEV 245
 DB 241 QSSLTRAVENTIQUEDNEISMLQEKEREFQEV 273

RESULT 12
 P79368

ID P79368 PRELIMINARY; PRT; 267 AA.
 AC P79368; Q28591;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE STEM CELL FACTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN NCBI_TaxID=9940;
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE-OVARIAN FOLLICLE;
 RX MEDLINE=96413880; PubMed=8662240;
 RA Tisdall D.J., Quirke L.D., Galloway S.M.;
 RT "Ovine stem cell factor gene is located within a syntenic group on
 chromosome 3 conserved across mammalian species.";
 RL Mamm. Genome 7:472-473(1996).
 RN [2]
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE-OVARIAN FOLLICLE;
 RA Tisdall D.J., Quirke L.D.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U89874; AAB49491.1; -.
 DR EMBL: 250743; CAA90620.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF, 1.
 FT NON_TER 267
 SQ SEQUENCE 267 AA: 30148 MW: 909D959E4B9EC841 CRC64;

Query Match 78.5%; Score 990.5; DB 6; Length 267;
 Best Local Similarity 74.2%; Pred. No. 1.4e-76;
 Matches 198; Conservative 19; Mismatches 21; Indels 29; Gaps 2;

QY 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNRVNNKVDYKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCIYIOLLFPNPLVKTGICRNPVDNDVITKLVANLPNDYMITLNYAG 60
 QY 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMNVOLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAKDFVVASETSDCVVSTLSPKSG----- 174
 QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 211
 DB 181 KPFMLPPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWKRR 240
 QY 212 QPSLTRAVENTIQUEDNEISMLQEK 238
 DB 241 KQPNLRTVENRQINEEDNEISMLQEK 267

RESULT 13

P97332 PRELIMINARY: PRT: 273 AA.
 ID 095MD2
 AC P97332: 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF S1-3NEU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=102/E1X3H/E1; Pubmed=9360640;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhäuser-Klaus, Pretsch;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
 RT gene defines a novel allele at the Steel locus with a weak
 RT phenotype."
 RL Mutat. Res. Genomics 382:75-78(1997).
 DR EMBL: Y10287; CAAT1329.1; --
 DR MGD: MGI:96974; K1L1.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 FT SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

Query Match 78.4%; Score 990; DB 11; Length 273;
 Best Local Similarity 72.2%; Pred. No. 1.6e-76;
 Matches 197; Conservative 18; Mismatches 30; Indels 28; Gaps 1;

QY 1 MKKTQWTLCTIYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPG 60
 DB 1 MKKTQWTLCTIYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPNDYMTTLNVA 60
 QY 61 MDVLPSCWISSEMYVOLSSTLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 120
 DB 61 MDVLPSCWISSEMYVOLSSTLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 120
 QY 121 KDLKSKFSPPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 DB 121 KDLKSKFSPPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 QY 121 KSIESPKRPPTSTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 180
 DB 121 KSIESPKRPPTSTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 212
 DB 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 212
 QY 213 OSLTRAVENIOINEEDNEISMLDKEKEREPOEV 245
 DB 213 OSLTRAVENIOINEEDNEISMLDKEKEREPOEV 245
 QY 241 OSLTRAVENIOINEEDNEISMLDKEKEREPOEV 273
 DB 241 OSLTRAVENIOINEEDNEISMLDKEKEREPOEV 273

RESULT 14

095MD2 PRELIMINARY: PRT: 261 AA.
 ID 095MD2
 AC 095MD2: 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MAST CELL GROWTH FACTOR (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey E.;
 RT "Equus caballus mast cell growth factor (MGF)."
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF401625; AAK94474.1; --

FT NON_TER 1 1
 FT NON_TER 261 261
 SQ SEQUENCE 261 AA; 29526 MW; 16A3062105346EAB CRC64;

Query Match 78.3%; Score 988.5; DB 6; Length 261;
 Best Local Similarity 75.5%; Pred. No. 2.1e-76;
 Matches 197; Conservative 19; Mismatches 16; Indels 29; Gaps 2;

QY 4 TQWTLCTIYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDV 63
 DB 1 TQWTLCTIYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDV 60
 QY 64 LPSHCWISSEMYVOLSSTLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 123
 DB 64 LPSHCWISSEMYVOLSSTLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 120
 QY 124 KSKFSKPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 DB 124 KSKFSKPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 QY 121 KSKFSKPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 180
 DB 121 KSKFSKPEPLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 214
 DB 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 214
 QY 215 SLTRAVENIOINEEDNEISML 235
 DB 215 SLTRAVENIOINEEDNEISML 235
 QY 241 NLTRAVENIOINEEDNEISML 261
 DB 241 NLTRAVENIOINEEDNEISML 261

RESULT 15

062765 PRELIMINARY: PRT: 256 AA.
 ID 062765
 AC 062765: 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN.
 RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
 RT "An Equine sequence homologous to stem cell factor (KIT-ligand)."
 RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF053498; AAC97076.1; --
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 FT NON_TER 1 1
 FT NON_TER 256 256
 FT SEQUENCE 256 AA; 28933 MW; 9EA876CAEC7B55FF CRC64;

Query Match 75.4%; Score 951.5; DB 6; Length 256;
 Best Local Similarity 75.0%; Pred. No. 2.8e-73;
 Matches 192; Conservative 18; Mismatches 17; Indels 29; Gaps 2;

QY 12 IYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDVLPSCWIS 71
 DB 1 IYQLLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDVLPSCWIS 60
 QY 72 EMVQHSVLSLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 131
 DB 72 EMVQHSVLSLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENS 120
 QY 132 PRFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 DB 132 PRFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKG----- 174
 QY 121 SLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKDSKVSATKPPMLPVAA 180
 DB 121 SLFTPEEFPRINRSIDAFKDFVASESDCVVSTLSPEKDSKVSATKPPMLPVAA 180

QY 175 -----KAKNPGDSSLIHWAMALPALFSLITIGFAGALYKKKROPSITRAVEN 222
Db 181 SSLRNDSSSSNRKASFTGDSNLOHAAALPAFFSLVIGFAFAGALYKKKOPNLTRAVER 240
QY 223 IQINEDNEISMLOEK 238
Db 241 IQINEDNEISMLOEK 256

Search completed: August 18, 2002, 13:06:06
Job time: 291 sec

